132, Appl 12, Appl 7, Appli 7, Appli 151, App 2, Appli 4, Appli

edinauce consideration of the consideration of the

ALIGNMENTS

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US-08-471-052A-132
US-08-189-331-132
US-08-471-939-132
US-08-471-068-132
US-08-471-068-132
US-08-449-644-7
US-08-906-769-151
US-08-906-769-151
US-08-906-769-151
US-08-906-769-151
US-08-91-955-4
US-08-91-955-4
US-08-91-955-4
US-08-997-362-135
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US-08-997-362-134
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
     CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-08-207-904-2
     Search time 9.32 Seconds (without alignments) 10.790 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-936-135-6
US-08-031-538-49
US-08-031-538-49
US-07-901-707-10
US-08-425-336-10
US-08-448-1138-10
US-08-477-4848-10
US-08-46-360-10
US-08-66-360-10
US-08-66-360-10
US-08-485-286-72
US-08-378-761A-81
US-08-378-761A-81
US-08-378-761A-81
US-08-356-405-2
US-08-356-405-2
US-08-356-405-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             164575 seqs, 16761186 residues
                                                                                                                                                                                   ٠.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                             October 20, 2000, 01:33:37
                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
                                                                                                                                                                                                                                                                               US-08-894-356C-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match
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                                                                                                                                                                                                                                                                               Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                   Sequence:
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                                                                                                                                                                             Run on:
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ö Gaps APPLICANT: Tuttle, Annwarie
APPLICANT: Tuttle, Lyle D.
TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
TITLE OF INVENTION: An Sequences and Recombinant DNA Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ö 100.3%; Score 40; DB 1; Length 448; 100.3%; Pred. No. 10; Cive 0; Mismatches 0; Indels MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC computible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,904
FILING DATE: CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/908,242
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LAZAT, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CGC 1624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 2: ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive Sequence 2, Application US/08207904 Patent No. 5477002 6; Conservative MOLECULE TYPE: protein Query Match Best Local Similarity Matches 6; Conserv 1 DFGWGK 6 US-08-207-904-2 à

Sequence Sequence Sequence S

Sequence Sequence

08-993-581B-8

-08-723-938-3 -09-080-538-3

Sequence

a

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77.5%; Score 31; DB 2; Length 45; 83.3%; Pred. No. 38; 1; Indels tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                 COMPUTER REALDABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA: 02/08/726,306A
FILING DATE: 02-0c-1996
PRIOR APPLICATION DATA: 02-0c-1995
PRIOR APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-0c-1995
PRIOR APPLICATION NUMBER: 38 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REGISTRATION NUMBER: 34,380
REGISTRATION NUMBER: 34,380
REGISTRATION NUMBER: 34,380
REGISTRATION NUMBER: 36,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN Rolease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
ITILE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESSONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DEBLISE DRIVE
CITY: HILLSBOROUGH
STATE: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08936135 Patent No. 6054293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFRENCE/POCKET NUMBER: UC97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 77.5
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: Single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-936-135-6
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                                                                                                         Sequence 17, Application US/08207904

Patent No. 5477002

GENERAL INFORMATION:

APPLICANT: Tuttle, AnnMarie

APPLICANT: Crossland, Lyle D.

TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic

TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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US-08-726-306A-51
Sequence 51, Application US/08726306A
Fatent No. 5958684
GENERAL INFORMATION
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INFORMION:
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: COMPACTION STATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/908,242

FILING DATE:

ATTORNEY AGENT INFORMATION:

NAME: Lazar, Steven R.

REGISTRATION NUMBER: 33,618

REFERENCE/DOCKET NUMBER: CGC 1624

TELECHONE: (919)541-8615

TELECHONE: (919)541-8619

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 448 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Havthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-207-904-17
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392 DFGWGK 397
392 DFGWGK 397
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                                                                    RESULT 2
US-08-207-904-17
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5 FGWGE 9
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APPLICANT: Statistics, J Gregor
APPLICANT: Statistics, Mark G
APPLICANT: Erlander, Mark G
APPLICANT: Lovenbarg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
                                                                                                                                                                                                                                                                                                                                          Length 923;
                                                                                                                                                                                                                                                                                                                     77.5%; Score 31; DB 3; Length 923
80.0%; Pred. No. 6.1e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIFTCATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Fiting, Thomas
RECISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR5099P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 2;
Pred. No. 41;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49, Application US/08031538; Patent No. 5968817; GENERAL INFORMATION:
TELEFAX: (650) 343-4342;
SEQUENCE CHARACTERISTICS:
LENGTH: 923 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: almoscid
TYPE: Almoscid
TYPE: Almoscid
TYPE: Almoscid
TYPE: Almoscid
TYPE: Peptide
US-08-936-135-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELERAX: 619-554-554 INFORMATION FOR SEQ ID NO: 49 SEQUENCE CHARACTERISTICS: 1.RNGTH: 33 aning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 75.0%;
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-031-538-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: La Jolla
STATE: CA
COUNTRY: USA
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651 EFGWG 655
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US-08-031-538-49
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Sequence 10, Application US/07901707

Patent No. 5376546

GENERAL INPORMATION:
APPLICANT: Berter, Marc J.
APPLICANT: Carroll, Steva F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray &
CORRESSE: Bickell:
ADDRESSE: Bickell:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                 APPLICANT: Britantion:
APPLICANT: Britander, Mark G
APPLICANT: Briander, Mark G
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS: ADDRESSEE: The SCTIPOS Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5958817th Torrey Pines Road, TPC 8
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 41;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTE: 7423,
COMPUTE: 7423,
COMPUTE: Floppy disk
COMPUTE: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/POCKET UNBER: 34,163
RELECOMMULCATION INFORMATION:
TELEPHONE: 619-554-2937
TURNDRANTYNE FOR STATEMENT OF STATEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two First National Plaza, 20 South Clark STREET: Street
Sequence 54, Application US/08031538
Patent No. 5968817
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%;
80.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 80.0
Matches 4; Conservative
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US-08-031-538-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA
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Length 33;

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Sequence 10, Application US/08425336
Patent No. 5621083
CENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF ENVENTION: Proteins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 1; Length 259;
Pred. No. 2.8e+02;
1; Mismatches 0; Indels
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-430-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MX-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-36,989
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
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83.3%;
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REGISTRATION NUMBER: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.0
Best Local Similarity 83.3
Matches 5; Conservative
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229 DFGFGK 234
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US-08-425-336-10
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APPLICANT: Bernhard, Susan L.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Chicago
STREET: Two first National Plaza, 20 South Clark
STREET: Illinois
COUNTRY: USA
ZIP: 60603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 30; DB 1; Length 259; 83.3%; Pred. No. 2.8e+02; tive 1; Mismatches 0; Indels
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37,302
REFERENCE/DOCKET NUMBER: 37,302
REFERENCE/DOCKET NUMBER: 37,303
TELEFONE: (312) 984-5750
TELEFONE: (312) 984-5750
TELERAX: 25-3856
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 anino acids
TODELOY: 110-ar
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
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FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/07988430 Patent No. 5416202 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.0 Best Local Similarity 83.3 Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-07-901-707-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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| 229 DFGFGK 234
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Gaps

Gaps

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Length 259;

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Sequence 10, Application US/OB477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Betret, Marc D.
APPLICANT: Studinks, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READALE FORM:
MEDIDID TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/477,484B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U$/08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U$ 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U$ 07/981,707
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: U$ 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: U$ 07/787,567
FILING DATE: 04-NOY-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/70-9155
TELEFONMUNICATION INPORMATION:
TELEPHONE: 312/70-9189
TELEFAX: 312/70-9189
TELEFAX: 550 388-1248
INPORMANION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: APPLICATION INDOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 1; Length 259; Pred. No. 2.8e+02;
                                                                                             Score 30; DB 1; 1
Pred. No. 2.8e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                    Query Match 75.0%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                     111:11
229 DFGFGK 234
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                     US-08-488-113B-10
                                                                                                                                                                                                                                                                                     RESULT 11
US-08-477-484B-10
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Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   ö
                                                                                                                                                                      Query Match
75.0%; Score 30; DB 1; Length 259;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN 1995
FILING DATE: 10-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/98,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1991
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
RESISTRATION NUMBER: 312/707-9155
TELEFAX: 650 388-1248
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LEMETH: 259 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: ALLORATOR: PROCEEDING
TYPE: ALLORATOR
TYPE: ALLORATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: McAndrews, Held & Malloy, Ltd. STREET: 500 West Madison Street, 34th floor
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acid
TYPE: amino acid
                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 500 West. CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                         111:11
229 DFGFGK 234
                                                                                                                                                                                                                                                                  1 DFGWGK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60661
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US-08-488-113B-10
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Gaps

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Indels

Mismatches

5; Conservative

Matches

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Sequence 10, Application PC/TUS9209487
Sequence 10, Application PC/TUS9209487
GENERAL INFORMATION:
APPLICANT: Berther, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 72, Application US/08378761A

Patent No. 563384

GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 259;
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Pred. No. 2.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
CITY: Lllinois
COUNTRY: USA
ZIP: 60603
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
FILING DATE: 19921104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19921104
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-010-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-N07-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 3133
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (312) 984-9740
TELES: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%;
83.3%;
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AMINO ACID
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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229 DFGFGK 234
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US-08-378-761A-72
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                                                                                                                                                                                                  Sequence 10, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 13
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Pred. No. 2.8e+02;
1; Mismatches 0; Indels
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SOCTAMRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSITICATION NUMBER: BCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: US 07/901,707
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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83.3%;
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LENGTH: 259 amino acids
TYPE: amino acid
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Best Local Similarity 83.3
Matches 5; Conservative
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MEDIUM TYPE: Floppy of
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229 DFGFGK 234
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229 DFGFGK 234
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Search completed: October 20, 2000, 01:35:57 Job time: 140 sec
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229 DFGFGK 234
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Sequence 72, Application US/08485286

Patent No. 5646026

Patent No.
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF TITLE OF INVENTION: USING NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRES T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 2.8e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 46268
COMPUTER HEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEDHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LESSONTH SOFT STATION:
TELEDHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LEBROTH: 200 amnino acids
TYPE: amino acid
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111:11
229 DFGFGK 234
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Pred. No. 2.8e+02;
1; Mismatches 0; Indels
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/378761
FILING DATE: 26-73N-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 38672B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 31-4846
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLLOGY: linear
NOLLECULE TYPE: protein
US-08-485-286-72
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1 DFGWGK 6
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2000, 01:34:22 ;
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T01056
S30515
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                                     T47886
A75486
T36369
I36787
T10173
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T46216
T10718
T10717
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T10719
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Compugen Ltd.
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              hypothetical prote
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ALIGNMENTS

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anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein - Arabidopsis thalian N;Alternate names: protein Filc1.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T45573
R;Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.: Mgwes, H.W.; submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23007
A;Accession: T45573
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 GBAR>
A;Cross-references: EMBL:AL132976
A;Experimental source: cultivar Columbia; BAC clone F11C1
                                                                              A; Map position: 3
A; Note: F11C1.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein - Arabidopsis thalian N;Alternate names: protein F1101.120
C;Species: Arabidopsis thaliana (mouse-car cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T45574
R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; A;Reference number: Z23007
A;Reference number: Z23007
A;Reference number: Z23007
A;Rocession: T45574
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-443 <ABAR>
A;Cross-references: EMBL:AL132976
A;Experimental source: cultivar Columbia; BAC clone F11C1
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A; Note: F11C1.120
             Query Match
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Similarity 100.0%;
6; Conservative 0
     100.0%;
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Pred. No. 8
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Length 450;

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probable anthranilate N-benzoyltransferase (EC 2.3.1.144) - muskmelon (fra N; Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase C:Species: Coucumis melo (muskmelon) C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-200 C; Accession: T09666 R; Aggelis, A.; John, I.; Karvouni, Z.; Grierson, D. Plant Mol. Biol. 33, 313-322, 1997 A:Title: Characterization of two cDNA clones for mRNAs expressed during ri A; Reference number: Z16810; MUID:97188564 A; Accession: T09666 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-455 <AGG> A; Cross-references: EMBL:Z70521; NID:e991794; PID:e234032 A; Experimental source: cultivar Cantaloupe charentals; pericarp of ripe fr C:Reywords: acvoltransferase: Cnenzyme A
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A;Experimental source: c
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A;Map position: 2
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(;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: (01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Apr-1999
C;Accession: T00527
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, Fi
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, E.A.; Crosby, M.L.; Brandon, Fi
Submitted to the EMBL Data Library, July 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence
A;Reference number: Z14167
A;Reference number: Z14167
A;Accession: T00527
A;Status: translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-451 <ROU>
A;Residues: 1-451 <ROU>
A;Residues: 1-451 <ROU>
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   hsr201 protein, hypersensitivity-related - common to:
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
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anthranilate N-benzoyltransferase-like protein - Arabidopsis thaliana N; Alternate names: protein F7J8.190 C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 C; Accession: T45961 R; Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewe submitted to the Protein Sequence Database, January 2000 A; Reference number: Z33018 A; Accession: T45961 A; Accession: T45961 A; Status: preliminary
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R;Czernic, P.; Huang, H.C.; Marco, Y.
Plant Mol. Biol. 31, 255-265, 1996
A;Title: Characterization of hsr201 and hsr515, two tobacco genes preferentially expr A;Reference number: Z14876; MUID:96343929
A;Accession: T03274
C; Genetics:
A; Map position:
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A; Residues: 1-475 <BEV>
A; Cross-references: EMB
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A; Gene: ATSP:F21B7.32
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
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A; Cross-references: EMBI
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                                                                                                                                       A:Description: catalyzes the synthesis of anthranilate A:Pathway: phytoalexin biosynthesis C:Keywords: acyltransferase; coenzyme A
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                                                                                                                                                                                                                                                                                                                                                         anthranilate N-benzoyltransferase (EC 2.3.1.144) (clone pchcbtla) - clove pink (fragment N;Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase C;Species: Dianthus caryophyllus (clove pink) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000 C;Accession: T10718 R;Yang, Q.; Reinhard, K.; Schiltz, E.; Matern, U.
                                                                                                                                                                                              A;Cross-references: EMBL:284384; NID:e1019563; PID:e294140 C;Function:
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                                                                                                                                                                                                                                                                                                                 R;Yang, Q.; Reinhard, K.; Schiltz, E.; Matern, R;Yang, Q.; Reinhard, K.; Schiltz, E.; Matern, Plant Mol. Biol. 35, 777-789, 1997
A;Title: Characterization and heterologous exp.
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A:Introns: 144/3
A:Note: T8P19.230
C:Superfamily: Arabidopsis
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A; Residues: 1-430 <CHO>
A; Cross-references: EMB
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000
C:Accession: T46216
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A; Accession: T46216
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DFGWG 393
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                                                             Conservative
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                                                        87.5%; Score 35;
100.0%; Pred. No.
Live 0; Mismatc
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Pred. No. 42;
1; Mismatches
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Pred. No. 9.4;
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A;Description: catalyzes the synthesis of anthranilate A;Pathway: phytoalexin blosynthesis C;Keywords: acyltransferase; coenzyme A
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A;Accession: T10719
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-445 < YAN>
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A;Title: Characterization and heterologous expression
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A:Molecule type: mRNA
A:Residues: 1-445 <YAN>
A:Cross-references: EMBL:Z84383; NID:e1019562; PID:e294139
C:Function:
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16-Jul-1999 #text_change 11-May-2000
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hypothetical protein YUP8H12R.39 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999
C;Accession: T01056
R;Theologis, A; Vysotskaia, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwan Oefner, P.; Davis, R.W.
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
A;Reference number: Z14227
A;Reference number: Z14227
A;Accession: T01056
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-572 <THE>
A;Cross-references: EMBL:AC002986; NID:g2494106; PID:g3152598; GSPDB:GN00059; ATSD:YUP8H
C;Gene: ATSP:YUP8H12R.39
A;Map position: 1
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A; Title: Anthranilate N-hydroxycinnamoyl/benzoyltransferase gene from carnation: Rapid A; Reference number: Z17092; MUID:99084770
A; Accession: T10711
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-446 <YAN>
A; Residues: 1-446 <YAN>
A; Cross-references: EMBL:Z98758; NID:e1309511; PID:e1309512
C; Function:
A; Description: catalyzes the synthesis of anthranilate
A; Pathway: phytoalexin biosynthesis
C; Keywords: acyltransferase; coenzyme A
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A;Molecule type: DNA
A;Residues: 1-485 <EDN>
A;Cross-references: EMBL:AF125442; PIDN:AAD12787.1; GSPDB:GN00022; CESP:H04M03.4
A;Experimental source: strain Bristol N2; clone H04M03
C;Genetics:
A;Gene: CESP:H04M03.4
A;Map position: 4
A;Introns: 40/3; 137/3; 258/3; 312/3; 376/3; 419/3
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R;Edwards, J.; Schaller, M.
submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid H04M03.
A;Reference number: 221425
A;Accession: T33865
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Search completed: October 20, Job time: 117 sec

2000, 01:36:19

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wound-induced protein - western balsam poplar C; Species: Populus trichocarpa (western balsam poplar) C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #te: C; Accession: S30515; S21011
R; Perkins, E.J.; Gordon, M.P.
submitted to the EMBL Data Library, November 1990
A; Description: Accumulation of two wound-responsive mRI
                       Qy
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                                                                                                        A;Molecule type: mRNA
A;Residues: 1-113 <PER>
A;Cross-references: EMBL:X56752; NID:g20964; PID:g20965;
                                                                                                                                                  A; Description: Accumulation of A; Reference number: S30515 A; Accession: S30515
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ALIGNMENTS

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EMBL; M65140; AAA51661.1;		license@isb-sib.ch).	requires a license agreement (See http://www.is	i and this statement is not removed. Usage by and for commerc	use by non-profit institutions as long as its content is in no way	opean Bioinformatics Institute. There are no restrictions on	ween the Swiss Institute of Bioinformatics and t	iss PROT entry is copyright. It is produced through	37.4.10.10.10.10.10.10.10.10.10.10.10.10.10.	TO THE PROPERTY OF THE PROPERT	THE HEXOL	WITH THE N-TERMINUS.	MINUS WHILE REGUI	CH OTHER	-!- SIMILARITY: THE N- AND C-TERMINAL HALVES OF THIS HEXOKINASE	IV (GLUCOKINASE).	PHOSPHORYLATING ISOENZYMES, DESIGNATED HEXOKINASE I, II, III AND	R GLUCOSE-		TTS HYDROPHOBIC N-TERMINAL SEQUENCE MAY BE INVOLVED IN MEMBRANE	CELLULAR LOCATION: BOUND TO THE OUTER MITOCHONDRIAL	- CUBONIT: MONOMER.	,	BY IT'S PRODUCT GLC-6-P.	REGULATION: HEXOKINASE IS AN ALLOSTER	:- CATALYTIC ACTIVITY: ATP + D-HEXOSE - ADP + D-HEXOSE 6-		function analysis.";	"Mammalian hexokinase 1: evolutionary conservation and structure to			; 92147096.			Biochem. Med. Metab. Biol. 41:125-131(1989).	08. 7	ligonucleotide primed amplification of cDNA using hi			_		SECUTION N.A.	[1] LOVINGE; BUS.	; Eucheria;	; metazoa; chordata; crantata; vertebrata; Euteleostomi;	(Bovine).		TYPE I (EC 2.7	l. 34, Last annotation	(Rel. 23, Last	(Rel. 23.	HARL BUYIN STANDARD; PRT; 918 AA.	BOVIN	JUT 1

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                                                                                                                                                                                                                                                   Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S. Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S., "Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAAO041-KIAAO080) deduced analysis of cDNA clones from human cell line KG-1."; DNA Res. 1:223-229(1994).

-I- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-I- SIMILARITY: BELONGS TO THE SKI2 SUBFAMILY OF HELICASES.
-I- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS INTRODUCED IN POSITION 837 TO MAKE THE PROTEIN LONGER AND MARKETING TO THE STATE OF THE SKI2 SUBFAMILY OF HELICASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y052_HUMAN
P42285;
                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              modified and this statement is not removed.
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00475; HEXOKINASE. PROSITE; PS00378; HEXOKINASES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P19:
INTERPRO;
 SEQUENCE
                                             Hypothetical protein; Helicase; ATP-binding; Nuclear protein
                                                                                                   INTERPRO;
                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL
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                                                                                         INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96051398.
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                              PF00270; DEAD; 1.
PF00271; helicase_C;
                                                                                                                D29641; BAA06124.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00349; hexokinase;
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PRO; IPR001312;
                                                                                                                                                                                                                                            SIMILARITY WITH SKI2.
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5; Conser
                                                                                         IPR001650;
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165
256
1045
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(Rel. 32, Last seq
(Rel. 35, Last ann
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476
149
597
84
532
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 118243
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                                                                                                                ALT_FRAME.
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CATALYTIC (BY SIMILARITY).
GLUCOSE-BINDING (POTENTIAL).
GLUCOSE-BINDING (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
DEIH
MW; 7
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                       ATP (POTENTIAL)
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7B16FF8E78049C20 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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67;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                          Query Match
Best Local :
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TKTC_CRAPL STANDARD;
Q42676;
Q1-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed entities requires a license agreement (See hor send an email to license agreement to the second entities and the second entities requires a license agreement to the second entitle the second enti
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mallet L., Bussereau F., Jacquet M.;

"A 43.5 kb segment of yeast chromosome XIV, which contains MFA2
MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 15.1 KDA PROTEIN IN RPC8-MFA2 INTERGENIC
YNL149C OR N1774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96109932.
Mallet L., Bussere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nasr F., Becam A.-M., Herbert C.J.;
"The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 complete open reading frames: 18 correspond to new genes, one of which encodes a protein similar to the human myotonic dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast 12:169-175(1996).
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Z71426; CAA96037.1;
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5; Conser
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5; Conserv
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Pred. No.
                                                                                                                                                                                                                                                                          Score 34;
Pred. No.
                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                             A1A41E3DA8CEAA06 CRC64;
                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                          18;
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74;
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MBL outstation -
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RESULT 5
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Best Local (
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SEQUENCE OF STRAIN-168;
                                                                                                                                                             TKT_BACSU STANDARD: PRT: 6
P45694:
01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
TRANSKETOLASE (EC 2.2.1.1).
TKT OR TKTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rehydration phase.";
EMBO J. 14:610-618(1995).
1- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE +
3-PHOSPHATE - D-RIBOSE 5-PHOSPHATE + D-XYLULOSE
1- COFACTOR: THIAMINE PYROPHOSPHATE.
1- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craterostigma plantagineum.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Euxaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Euxaryota; Virinhvta; eudicotyledons; core eudicots; Asteridae; euasterids
                                                     Rose M., Entian K.;
Submitted (JUN-1996)
                                                                                                                                   Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Thiamine pyrophosphate; Chloroplast; Multigene NON_TER 1 1 1 SEQUENCE 519 AA; 56187 MW; 7AFD034CE2EC5685 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: CHLOROPLAST (POTENTIAL).
-i- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN
-i- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bernacchia G., Schwall G., Lottspeich F., Salamini F., Bartels "The transketolase gene family of the resurrection plant Craterostiqma plantagineum: differential expression during the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
01-NOV-1997
                                                                              STRAIN-168;
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00801; TRANKETOLASE_1; PARTIAL. PROSITE; PS00802; TRANKETOLASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                        Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPRO00360; -.
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                                                                                                                                                                                                                                                                                                                    473 FGWGK 477
                                                                                                                                                                                                                                                                                                                                             2 FGWGK 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00456; transketolase;
                                                                                                                                                                                                                                                                                                                                                                         Similarity
5; Conserv
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 Yon
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                           561-667 FROM N.A.
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el. 35, Last annotation update)
CHLOROPLAST (EC 2.2.1.1) (TK) (FRAGMENT).
Wachenfeldt C.,
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Pred. No.
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Hederstedt L.;
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5-PHOSPHATE.
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RESULT 6
VG17_HSVI1
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EMBL; 287845; CAA61113.1; -.
EMBL; 299113; CAB13673.1; -.
HSSP; P23254; 1AVO
SUBTILIST; BG11247; TKT.
INTERPRO; IPRO00360; -.
                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992
01-DEC-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                             VG17_HSVI1
Q00116;
                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM: PF00456; transketolase; 1.
PROSITE; PS00801; TRANKETOLASE_1; 1.
PROSITE; PS00802; TRANKETOLASE_2; 1.
Transferase; Thiamine pyrophosphate.
SEQUENCE 667 AA; 72344 MW; D93BCACD246148AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                    יבייי, שאטעא viruses, no RNA stage; Herpesviridae; unclassified Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE

- 3-PHOSPHATE - D-RIBOSE 5-PHOSPHATE + D-XYLULOSE 5-PHOSPHATE.

- 1- COFACTOR: THIAMINE PYROPHOSPHATE.
                          EMBL; M75136; AAA88120.1; PIR; I36787; I36787.
                                                                                                                                                                                                                                                                                                                                Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Hypothetical protein SEQUENCE 298 AA;
                                                                                                                                                                                                    "Channel catfish virus: a new type of herpesvirus."; virology 186:9-14(1992).
                                                                                                                                                                                                                                   Davison A.J.;
                                                                                                                                                                                                                                                  MEDLINE; 92087490.
                                                                                                                                                                                                                                                                 STRAIN-AUBURN
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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5; Conserv
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L GENE 17 PROTEIN.
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MW;
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4C90B1DEEA203FA9 CRC64;
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Query Match Best Local

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RESULT 8
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Q57845;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Xaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Compacibit "...
  SEQUENCE FROM N.A. MEDLINE; 97454242. McWhirter J.R., Go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67492; AAB98395.1; TIGR; MJ0402; -.
                                                                                                                                                                                                                 15-JUL-1999 (Rel.
15-JUL-1999 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                         FGFF_MOUSE 035622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-JAL-1 / DSM
MEDLINE; 96337999.
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                                                                                                 Mammalia;
                                                                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                         FGF15
                                                                                                                                                                                                FIBROBLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence 
jannaschii.";
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67 NFGWGR 72
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                                                                                              Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l protein.
106 AA; 12600 MW;
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                                                                                                                                                                                                                                                                                                                  STANDARD;
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Goulding
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                                                                                                                                                                                             FACTOR-15
                                                                                       Chordata; (
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80.0%;
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Pred. No. 48;
  Weiner
                                                                                                                     Craniata; Vertebrata;
                                                                                              Sciurognathi;
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                                                                                                                                                                                                                                                                                                                  218
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Chun
                                                                                                 Muridae;
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                  OPSR_CANFA STANDARD; PRT; 273 AA 0.18914; 273 Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                            Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                               CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                   -
                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                           RED-SENSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oncoprotein E2A-Pbx1.";
Development 124:3221-3232(1997)
                                                         +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00262; IL1HBGF.
PROSITE; PS00247; HBGF_FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A novel fibroblast growth factor gene expressed in the developing
nervous system is a downstream target of the chimeric homeodomain
                                                                                                                                                                                                               Yokoyama S., Radlwimmer F.B.;
"The 'five-sites' rule and th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GD; MG1:10>0000; -.
INTERPRO; IPRO02209; -.
INTERPRO; IPRO02348; -.
INTERPRO; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FGWGK 6
:||||
44 YGWGK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity ues 4; Conserv
                                                                                               MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALE LINKED TO CIS-RETINAL. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. TISSUE SPECIFICTY: THE THREE COLOR PTOMPSUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND PATTERNING WITHIN SPECIFIC REGIONS O. SPINAL CORD AND SENSORY ORGANS.
SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: EXPRESSED IN THE DESTRIBUTION: REFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY
                                         OPSIN SUBFAMILY.
                                                         SIMILARITY: BELONGS
                                                                                   PHOTORECEPTOR CELLS. PTM: SOME OR ALL OF
                                                                      BE PHOSPHORYLATED
SWISS-PROT entry is copyright. It is produced through a collaboration sen the S_w is Sinstitute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                        98242086
                                                                                                                                                                                                                                                        FROM N.A.
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218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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OPSIN (RED CONE PHOTORECEPTOR P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
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25236 MW;
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                                                                                   CARBOXYL-TERMINAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. FIBROBLAST GROWTH FACTOR-15.
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                                                         G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                    Euteleostomi;
Canis.
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                                                                                                            FOUND IN THE CONE
                                                                                     RESIDUES MAY
                                                                                                                                                       COVALENTLY
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AC P47231;
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DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BIPHENYL-2,3-DIOL 1,2-DIOXYGENASE I (EC 1.13.11.39)
AVYGENASE I) (2,3-DIHYDROXYBIPHENYL DIOXYGENASE I)
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DOMAIN 1

TRANSMEM 6

DOMAIN 31

TRANSMEM 43

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TRANSMEM 12

DOMAIN 103

TRANSMEM 12

DOMAIN 146

TRANSMEM 172

DOMAIN 202

DOMAIN 203

TRANSMEM 279

DOMAIN 246

TRANSMEM 254

DISULFID 79
Asturias J.A., Ettis L.D., Prucha M., Timmis K.N.;

*Analysis of three 2,3-dihydroxybiphenyl 1,2-dioxygenases found in Rhodococcus globerulus p6. Identification of a new family of extradiol dioxygenases.*,

J. Biol. Chem. 269:7807-7815(1994).

-I- CATALYTIC ACTIVITY: BIPHENYL-2,3-DIOL + O(2) = 2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIEMOATE + H(2)O.

-I- COPACTOR: FERROUS ION.

-I- PATHWAY: DEGRADATION OF BIPHENYLS AND PCLYCHLOROBIPHENYLS (PCB) BENNOIC ACID AND CHLOROBENZOIC ACIDS.

-I- SIMILARITY: BELONGS TO THE EXTRADIOL RING-CLEAVAGE DIOXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM DISULFID BINDING NON_TER SEQUENCE
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INTERPRO; IPR001760; -.
PFAM; PF00001; 7tm_1; 1.
                                                                                                                                        MEDLINE;
                                                                                                                                                 STRAIN-P6;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                      Actinomycetales;
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CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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P17297; Q52441;
Q1-AUG-1990 (Rel. 15, Cr
Q1-NOV-1995 (Rel. 32, La
15-JUL-1999 (Rel. 38, La
BIPHENYL-2,3-DIOL 1,2-DI
(2,3-DIHYDROXYBIPHENYL D
                                                                                                                                               complexes of an example of the property of the
                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96226036.
Senda T., Sugiyama K., Narita H., Sato M., Yano K., Mitsui Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and sequencing of two tandem genes involved in degradation of 2,3-dihydroxybiphenyl to benzoic acid in the polychlorinated biphenyl-degrading soil bacterium Pseudomonas sp. strain KKS102."; Bacteriol. 171:2740-2747(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF01013; EXTRADIOL_DIOXYGENAS; 1.
PROSITE; PS00082; EXTRADIOL_DIOXYGENAS; 1.
OX1doreductase; Dioxygenase; Aromatic hydric METAL 146 146 1700 (BY SIMI)
METAL 210 210 170N (BY SIMI)
METAL 260 260 170N (BY SIMI)
METAL 260 260 170N (BY SIMI)
                                                                                                                                                                                                                                                                                              "Three-dimensional structures of free form and complexes of an extradiol ring-cleavage type dienzyme from Pseudomonas sp. strain KKS102.";
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                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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HSSP; P47228; 1HAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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32, Last sequence update)
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1,2-DIOXYGENASE (EC 1.13.11.39) (230HBP OXYGENASE)
PHENYL DIOXYGENASE) (DHBD).
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01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 31, Last sequence update)
15-JUL-1989 (Rel. 11, Created)
15-JUL-1989 (Rel. 11, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dloxygenase gene from the PCB-degrading strapaucinobilis Q1.",
Biochemistry 27:3990-3996(1988).
-1- CATALYTIC ACTIVITY: BIPHENYL-2,3-DIOL +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M26433; AAA25750.1;
EMBL; D17319; BAA04141.1;
PIR; A32312; DAPSPC.
PDB; 1DHY; 15-OCT-95.
  EMBL; M20640; AAA25678.1;
PIR; A28718; A28718.
HSSP; P17297; 1DHY.
                                                                                                                                                                   use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
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PROSITE; PS00082; EXTRADIOL_DIOXYGENAS; 1

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MEDLINE: 97443975.

Link A.J., Robison K., Church G.M.;

Link A.J., Robison K., Church G.M.;

Comparing the predicted and observed properties of p
in the genome of Escherichia coli K-12.";

Electrophoresis 18:1259-1313 (1997).

-1- CATALYTIC ACTIVITY: 2 S-ADENOSYL-L-METHIONINE + U

-2 S-ADENOSYL-L-HOMOCYSTEINE + SIROHYDROCHLORIN.

-1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF SIROHEME
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                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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01-MAR-1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE UROPORPHYRIN-III C-METHYLTRANSFERASE
                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entry of 
                                                                                                                                                                                                                                                                                                                                                                                                                       Daniels D.L., Plunkett G. III "Analysis of the Escherichia from 84.5 to 86.5 minutes.", Science 257:771-778(1992).
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"The sequence of hemC,
Nucleic Acids Res. 16:
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"Nucleotide sequence of the hemX gene, to
operon of Escherichia coli K12.";
Nucleic Acids Res. 16:11835-11835(1988).
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GLYCCOGEN SYNTHASE (
                                                                                                                                                                                                                                                                                     "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rnB-dnaB region.";
Microbiology 143:3431-3441(1997).
-!- FUNCTION: SYNTHESIZES ALPHA-1,4-GLUCAN CHAINS USING ADP-GLUCOSE.
-!- CATALYTIC ACTIVITY: ADP-GLUCOSE + (1,4-ALPHA-D-GLUCOSYL)[N] - ADI + (1,4-ALPHA-D-GLUCOSYL)[N+1].
-!- PATHWAR: SECOND STEP IN GLYCOGEN BIOSYNCHESIS.
-!- INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON SOURCES THAT ALLOW EFFICIENT SPORULATION.
-!- SIMILARITY: BELONGS TO THE BACTERIAL OF THE PAMILY
  EMBL;
EMBL;
                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                operon encoding degradation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kiel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLGA_BACSU
P39125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECO2DBASE; B043.0; 6TH EDITION.
ECO2DBASE; B043.1; 6TH EDITION.
ECOGENE; EG10433; HEMX.
Porphyrin blosynthesis; Transferase; Methyltransferase.
Porphyrin blosynthesis; Transferase; Methyltransferase.
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EMBL;
EMBL;
EMBL;
PIR;
PIR;
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Bacteria; Firmicutes;
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"Glycogen in Bacillus
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                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGWGK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiol.
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                                              Z25795; CAA81043.1; -.
                        AF008220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
  CAB15073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boels J.M., Beldman G., Venema G.; cillus subtilis: molecular characterization of enzymes involved in glycogen biosynthesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11:203-218(1994).
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38,
38,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.M.,
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Last annotation update)
2.4.1.21) (STARCH [BACTERIAL GLYCOGEN]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Clostridium group;
us group; Bacillus.
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Pred. No. 1.5e+02,
1; Mismatches (
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Best Local S
Matches 4
                                                                                                                                                                  CHARACTERIZATION.
MEDLINE; 91355206.
WOLZ R.L., Harris R.B., Bo
"Mapping the active site o
inhibitors.";
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SUBTILIST: BG10910; GLGA
Glycogen biosynthesis; T
BINDING 1 15
SEQUENCE 484 AA; 5585
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P28825;
01-DEC-1992
01-NOV-1997
                                                                                                                                                                                                                                            "Jiang W., Flannery A.V.;
"Correlation of the exon/intron organization to the secondary structures of the protease domain of mouse meprin alpha subungene 189:65-71(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U1-NOV-1997 (Rel. 35, I
15-JUL-1998 (Rel. 36, I
MEPRIN A ALPHA-SUBUNIT
                                                                                                                                                      Biochemistry 30:8488-8493(1991)
                                                                                                                                                                                                                                                                                                        STRAIN-129;
                                                                                                                                                                                                                                                                                                                                             Dumermuth E., Sterchi E.E., Jiang W., Wolz R.L. Flannery A.V., Beynon R.J.;
"The astacin family of metalloendopeptidases.";
J. Biol. Chem. 266:21381-21385(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PART
STRAIN-C57BL/6, AND C3H/HE;
MEDLINE; 92250517.
MEDLINE; 9250517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                           MEDLINE; 97305147.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 64-247 FROM N.A. MEDLINE: 92042028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           differential expression
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COFACTOR: BINDS ONE ZINC ION.

COFACTOR: BINDS ONE ZINC ION.

SUBUNIT: HOMOTETRAMER OF ALPHA OR BETA SUBUNITS; HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS ARE FORMED BY NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED HETERODIMERS; GENETIC FACTORS DETERMINE WHICH OLIGOMER(S) WILL BE FORMED (STRAIN-SPECIFIC).

SUBCELLULAR IOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: KIDNEY, INTESTINAL BRUSH BORDERS, AND SALIVARY DUCTS.

PTM: N-GLYCOSYLATED; AT LEAST 3 OF THE POTENTIAL SITES ARE USED.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                           CATALYTIC ACTIVITY: HYDROLYSIS (
PREFERENTIALLY ON CARBOXYL SIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYSWGK 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ial expression in inbred mouse st
evolution of the alpha and beta
Chem. 267:9185-9193(1992).
                                                                                                                                                                                                                                                                                                                    62-258
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. 36, Last anno
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Last annotation update)
T PRECURSOR (EC 3.4.24.18)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flannery
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e of n
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Pred. No. 1.8e
1; Mismatches
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                                                                                                                                                                              meprin-A with
                                                                                                                                                                                         J.S.;
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Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.V.,
                                                                                                                        OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           747
                                                                                                                           PROTEIN AND I
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C RESIDUES.
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evidence for
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PRINTS; PRO0480; ASTACIN.

PROSITE; PS000142; ZICC_PROTEASE; 1

PROSITE; PS00740; MAM_1; 1.

PROSITE; PS00060; MAM_2; 1.

PROSITE; PS00060; MAM_2; FALSE_NEG

PROSITE; PS001186; EGF_2; FALSE_NEG
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PDB: IIAF: 31-AUG-94.

MGD: MGI:96963; MEP1A.

INTERPRO: IPRO00130; -

INTERPRO: IPRO00551; -

INTERPRO: IPRO00599; -

INTERPRO: IPRO002083; -

INTERPRO: IPRO02083; -

PEAM: PF01400; Astacin; 1.

PEAM: PF00008; EGF: 1.

PEAM: PF000629; MAM: 1.

PEAM: PF00629; MAM: 1.
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COMAIN
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SIGNAL
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EMBL; U62765; AAC53194.1; -.
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        565
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
1:111:
DWGWGQ 570
                                                         DFGWGK 6
                                                                                                          l Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal
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50060; MAM_2; 1.
500020; EGF_1; FALSE_NEG.
501186; EGF_2; FALSE_NEG.
Metalloprotease; Zinc; Glycoprotein; Transmembrane;
Metalloprotease; Zinc; Glycoprotein; Transmembrane;
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                       Score 31; DB 1; L
Pred. No. 2.6e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                       N-LINKED (GLCNAC.
T -> A (IN REF. 2)
; 2A18242A43505633
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EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
METALLOPROTEASE.
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                          Length 747;
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                                                                                                                                                                                                                                                                                        (POTENTIAL)
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Search completed: October 20, 2000, 01:37:07 Job time: 115 sec

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Result
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Maximum DB seq
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1: /SIDS6/gcgda*

2: /SIDS6/gcgda*

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(c) 1993 - 2000 Compugen Ltd
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                                                              Aromatic acyl tran
C. roseus DAT prot
Aromatic acyl tran
Polypeptide encode
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Aromatic acyl tran
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ALIGNMENTS

RESULT W04728

W04728 standard; Protein; 6 AA.

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30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
 DNA coding for aromatic acyl transferase -
                                                                                                                                                                                                                           Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia.
                                                                                                                                                                                                                                                                                                        06-FEB-1997 (first entry)
                                        Ashikari T, Fujiwara H, Fukui
Nakao M, Tanaka Y, Yonekura K;
                                                                                                                                         16-FEB-1996;
                                                                                                                                                                                   W09625500-A1.
                                                                                                                                                                                                         Gentiana triflora var. japonica (Clone pGAT4).
                                                                                                                                                                                                                                                                                   Aromatic acyl transferase peptide fragment.
                                                                                                                                                                                                                                                                                                                                W04728;
                      WPI; 1996-393401/39.
                                                                                                                                                               22-AUG-1996.
                                                                         (SUNR ) SUNTORY LTD.
                                                                                              96JP-0046534.
95JP-0067159.
95JP-0196915.
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for transforming plants
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Best Local
This invention describes a novel consensus sequence (I) for the identification of acyltransferase enzyme in plants. (I) comprises His-X_1-X_2-X_3-Asp-X_4 where X_1 = an amino acid comprising Ala, Arg, Thr. Cys, Asn, His, Met, Ile, Leu, Val or Lys; X_2 = an amino acid comprising Val, Ile, Leu or Met; X_3 = an amino acid comprising Cys, Phe, Val, Leu, Met, Ala, Gly, Ser or Thr; and X_4 = an amino acid comprising Gly, Ala, Ile, Met or Val. The invention also describes a novel method for the identification of acyltransferase enzyme in plants comprising: (a) the steps of (i) DNA amplification using PCR primers specific for (I) coupled to 3'- or 5'- RACE (rapid amplification of cDNA ends) protocols; (ii) direct screening of cDNA and genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. roseus
                                                                                                                                                                  Disclosure; Fig 2; 57pp; English.
                                                                                                                                                                                            acyltransferase enzymes
                                                                                                                                                                                                                                                             St-Pierre B,
                                                                                                                                                                                                                                                                                                                                                                                                                          Catharanthus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313. This peptide fragment was isolated from three of the six clones and was used synthesise a degenerate primer (T37314) which was then used to identify other aromatic acyl transferase encoding clones.
                                                                                                                                                                                                             Novel
                                                                                                                                                                                                                                                                                       ( -OMYD)
                                                                                                                                                                                                                                                                                                                  10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                           10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acyltransferase; plant; RACE; screening; anti-DAT antibody; DAT; deacetylvindoline 4-0-acetyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y51247 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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  of flowers
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ransferase enzymes in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and thus altering colour tone,
                                                                                                                                                                                                          useful for the identification
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hes 0;
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Best Local S
Matches 6
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17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                                                                                                                                          DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 open reading frame encourny a process and 54kDa. This sequence represents which is described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             libraries using degenerate primers based on (I); (iii) screening of cDNA expression libraries using antibodies specific for (I); or (iv) screening of cDNA expression libraries using anti-DAT (deacetylvindoline 4-O-acetyltransferase) antibodies; (b) identifying in clones of (I); (c) identifying homology to the DAT gene family; and (d) identifying an open reading frame encoding a protein with a molecular weight between 45
                                                    tone changes and allowing new colourations to be produced specific DNA sequences encoding aromatic acyl transferase different plants are described in T37308-T37313.
                                                                                                                  Vectors containing DNA fragments encoding proteins of plant cwith aromatic acyl transferase activity may be used to transferants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W04725 standard;
                                                 different
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aromatic acyl transferase of Perilla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashikari T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9625500-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scenecio cruentus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plants; acylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aromatic acyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 dfgwgk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DFGWGK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w
                                                                                                                                                                                                                                               4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z,
                                                                                                                                                                                                                                                                                                                                                                                             T37311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conser
                                                                                                                                                                                                                                               Page 65-68; 94pp;
                                                 plants are described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiwara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96JP-0046534.
95JP-0067159.
95JP-0196915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-JP00348
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĸ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Clone pSAT208)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colour; tone; colouration; colour colour colour petunia hybrida; perilla ocimoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lavandula angustifolia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yonekura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukui
                                                                                                                                                                                                                                               Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Catharanthus roseus DAT protein the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kusumi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocimoides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anthocyanin pigment;
                                                                                                                                                The aromatic acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colour change;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mizutani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                plant origin
                                                                                                                                                                       transform
                                                                          from
                                                                                                                                                                                                                                                                                                                     plants
tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                          colour
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Sequence

446

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RESULT
RAYA775
                                                                                                                                                                                                                Anther specific cDNA or genomic sequences can be used to identify and isolate anther specific promoters. The anther specific promoter can then be cloned into a recombinant construct and used to express theterologous genes. Preferred heterologous genes include Diptheria chrysanthemi; T-urfl3 from cms-T maize mitochondrial genomes; the chrysanthemi; T-urfl3 from cms-T maize mitochondrial genomes; the chrysanthemi; T-urfl3 from cms-T maize mitochondrial genomes; the cynthetase gene from page Mu; the indole acetic acid-lysine crom Bacillus thuringiensis Israeliensis. All of these genes when campaignessed in anther tissue will result in the inability of the plant to produce viable pollen. Transformation of plants with such can recombinant construct can produce transgenic, male sterile plants. Can be sterillty is important in the production of hybrid seeds as it prevents self pollination which hinders breeding and hybrid seed
                                                    Matches
                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 25-27; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anther-specific cDNA, genomic and recombinant DNA - produce transgenic male-sterile plants, which prevents self-pollination,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in hybrid seed prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crossland LD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic plants; male sterility; pollen; self-pollination; seed; hybrid; toxin-A; pe CytA; toxin; Nicotiana tabacum; Diptheria; phage Mu; Psuedomonas syringae; Bacillus th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1994
                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R47475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R47475 standard; Protein;
1 DFGWGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||
| 389 dfgwgk 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DFGWGK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1994-010428/02
                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q54685,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6,
                                                                                                                                                                      448
σ
                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuttle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93EP-0810455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-0908242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q53693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anther specific cDNA clone ant32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
                                                            Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB
Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Å
                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diptheria; Erwinia chrys
Bacillus thuringiensis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ry; pollen; sterile; toxin-A; pelE; T-urfl3; Gin; iaa; toxin-A; pelE; T-urfl3; Gin; iaa; biptheria; 3rwinia Chrysanthemi;
                                                            19;
                                                                                   DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
19;
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                                                                              Length 448;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iaaL;
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                          Gaps
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                          0
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Petunia hybrida (Clone pPAT48).

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R46929
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                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                Query Match
Best Local
       Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia.
                                                            Aromatic acyl
                                                                                                  W04724;
                                                                               06-FEB-1997
                                                                                                                  W04724 standard;
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                              polymerase gene or to GALA/VPI fusion gene in order to produce male-sterile plants. The inventors claim that male-sterile plants finally produced can be used to increase hybrid vigour in plants, e.g. maize.
                                                                                                                                                                                                                                                                                                   R46929 is anther specific from Nicotiana tabacum. The ant32 promoter can be operably linked to, eg
                                                                                                                                                                                                                                                                                                                                                 Dual method for producing male-sterile plants - comprises crossing 2 genetically transformed plants, useful for producing hybrid seed
                                                                                                                                                               392 dfgwgk 397
                                                                                                                                                                                                                                                                                                                                   Example 8; Page 22-28;
                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q58340.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-119827/15.
                                                                                                                                                                                                                                                                                                                                                                                                                      Crossland LD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP589841-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (CIBA ) CIBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobacco ant32 genomic protein; male-sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R46929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R46929 standard;
                                                                                                                                                                                                     Local Similarity es 6; Conserv
                                                                                                                                                                                   1 DFGWGK 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dfgwgk 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ant32
                                                                                                                                                                                                                                                  448 AA;
                                                                             (first entry)
                                                                                                                                                                                                    Conservative
                                                        transferase of Petunia hybrida.
                                                                                                                                                                                                                                                                                                                                                                                                                                       GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic
                                                                                                                                                                                                                                                                                                                                                                                                                     Stein JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0950348.
                                                                                                                  Protein; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93EP-0810654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone
                                                                                                                                                                                                                                                                                                                                                                                                                    Tuttle A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448
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                                                                                                                                                                                                           Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded sequence.
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                  Length 448;
                                                                                                                                                                                                                                                                                                    T7
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RESULT WOATZT ID WATZT ID WATZ
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashikari T, ruj-
                                                                                                                                                                                                                                                                                                                   Aromatic acyl transferase; transformation; anthocyanin pigme plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W04727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour
                                           16-FEB-1996;
                                                                                                                                    WO9625500-A1
                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                             Lavandula
                                                                                                                                                                                                                                                                                                                                                                                                                                         Aromatic acyl transferase of Lavadula angustifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-FEB-1997
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                                                                                        22-AUG-1996
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| dfgwgk 395
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                                                                                                                                                                                                                                                                          angustifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 AA;
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95JP-0067159.
95JP-0196915.
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                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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Yonekura K;
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19;
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RESULT
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         Ashikari T, Fuji
                                                                                                                                30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which produce anthocyanin pigments and the e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313. NOTE: This sequence is supposed to cross reference with the nucleotide described in T37313, however there are so many discrepancies between the polypeptide decoded from that sequence and this polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                               Aromatic acyl transferase; transformation; anthocyanin pigme plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
                                                                                                                                                                                                                                                                       22-AUG-1996
                                                                                                                                                                                                                                                                                                                    WO9625500-A1
                                                                                                                                                                                                                                                                                                                                                               Senecio cruentus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 73-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-393401/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashikari T, Fuji
Nakao M, Tanaka
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29-JUN-1995;
                                                                                       (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                          16-FEB-1996;
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393 dfgwgk 398
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nes 6; Conserv
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                  Fujiwara H, Ful
naka Y, Yonekura
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naka Y, Yonekura
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95JP-0067159.
95JP-0196915.
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95JP-0196915
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                                                                                                                                                                                                                                                                                                                                                                 (Clone
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                                                                                                                                                                                                                                                                                                                                                               pcate).
                     Fukuí
kura K;
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ura K;
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tone,
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RESULT
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Best Local :
Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl
                                                                                                     Claim 4; Page 53-57; 94pp; Japanese
                                                                                                                                                   DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                                                                                                                                                                                       Nakao
                                                                                                                                                                                                                                                                                                                                                             Ashikari
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                                                                                                                                                                                                                                                                                                                                                                                                           (SUNR ) SUNTORY LTD.
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N-PSDB; T37312.
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DB; T37308.
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1. Tanaka Y,
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naka Y, Yonekura K;
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95JP-0067159.
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Pred. No.
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Best Local S
Matches 6
         Vectors containing DNA fragments encoding proteins of plant origin with arcmatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The arcmatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding arcmatic acyl transferase from different plants are described in T37308-T37313.
 Sequence
                                                                                                                                                                                                                                                                         30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
                                                                                                         Claim 4; Page 57-61; 94pp; Japanese.
                                                                                                                                     DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
                                                                                                                                                                                   WPI; 1996-393401/39.
N-PSDB; T37309.
                                                                                                                                                                                                                    Nakao M,
                                                                                                                                                                                                                               Ashikari
                                                                                                                                                                                                                                                                                                                       16-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                    Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia.
                                                                                                                                                                                                                                                   (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                             22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                   W09625500-A1
                                                                                                                                                                                                                                                                                                                                                                                         Gentiana triflora
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aromatic acyl transferase of Gentiana triflora var. japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W04723 standard; Protein; 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W04723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313.
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Tanaka
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AA.
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95JP-0067159.
95JP-0196915.
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                                                                                                                                                                                                                                                                                                                                                                                  var. japonica (Clone pGAT106).
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Query Match Best Local S Matches 6

Similarity 6; Conserv

100.0%; llarity 100.0%; Conservative 0;

Score 40; Pred. No.

20; DB 17;

Length 479; Indels

Mismatches

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RESULT 11
Y51235
RESULT
Y68644
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Best Local Similarity
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising Val, Ile, Leu or Met; X_3 = an amino acid comprising Cys, Phe, Val, Leu, Met, Ala, Gly, Ser or Thr; and X_4 = an amino acid comprising Gys, Ala, Ile, Met or Val. The invention also describes a novel method for the identification of acyltransferase enzyme in plants comprising; (a) the steps of (i) DNA amplification using PCR primers specific for (I) coupled to 3' or 5' - RACE (rapid amplification of CDNA ends) protocols; (ii) direct screening of CDNA and genomic ilbraries using degenerate primers based on (I); (ii) screening of CDNA expression libraries using antibodies specific for (I); or (iv) screening of CDNA expression libraries using antibodies specific for (I); (v) identifying homology to the DAT gene family; and (d) identifying an open reading frame encoding a protein with a molecular weight between 45 and 54kDa. This sequence represents a plant acyl-transferase conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catharanthus
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel consensus sequence (I) for the identification of acyltransferase enzyme in plants. (I) comprises His-X_1-X_2-X_3-Asp-X_4 where X_1 = an amino acid comprising Ala, if it is a maniferation of a cyltransferation and in the comprising Ala, if it is a maniferation acid comprising the compression and in the cylindrical compression and in the cylindrical compression and in the cylindrical compression acid compression acid compression acid compression acid cylindrical compression and cylindrical compression acid cylindrical cyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. roseus acyl-transferase conserved peptide motif #2.
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5 dfgwgk 420
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54kDa. This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 4; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                    10 AA;
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                                                                                                                                                                                                                           Conservative
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especially where repeated delivery is required. Adenoviruses of the invention are useful can be constructed to have a desired host range and a diminished capability to raise neutralizing antibodies, an absence of, or decreased infection of, antigen presenting cells of the immune system (e.g. macrophages), and an ability to escape trapping in the liver through increased target cell specificity.
                                                                                                       chimaeric adenoviruses with reduced antigenicity. The chimaeric adenoviruses comprise at least part of a fiber protein of an adenovirus serotype providing the chimaeric virus with a desired host range and at least part of a penton or hexon protein from another, less antigenic, serotype. The chimaeric adenoviruses are useful for gene therapy,
                                                                                                                                                                         Y68642-70 represent the amino acid sequences of the fiber proteins of Adenovirus serotypes 8, 9, 13, 14, 20, 23, 24, 25, 27, 28, 29, 30, 32, 33, 34, 35, 36, 37, 38, 39, 42, 43, 44, 45, 46, 47, 48, 49 and 51. The proteins are used in the course of the invention to construct
                                                                                                                                                                                                                                                                       New chimaeric adenoviruses containing a genome derived adenovirus serotypes, useful in gene therapy - {\sf res}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                             Example 2;
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                                                                                                                                                                                                                                                                                                                                                                    (INTR-) INTROGENE BV.
                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1998;
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                   macrophages), and macrophages
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Sequence

Query Match Best Local 9

Similarity 5; Conser

Conservative

87.5%;

Score 35; DB 21; Pred. No. 1.1e+02; 1; Mismatches 0

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                        Query Match
Best Local Similarity 83.
Matches 5; Conservative
                                                                                                                                                                                  Y68642-70 represent the amino acid sequences of the fiber proteins of Adenovirus serotypes 8, 9, 13, 14, 20, 23, 24, 25, 27, 28, 29, 30, 32, 33, 34, 35, 36, 37, 38, 39, 43, 44, 45, 46, 47, 48, 49 and 51. The proteins are used in the course of the invention to construct chimaeric adenoviruses with reduced antigenicity. The chimaeric adenoviruses comprise at least part of a fiber protein of an adenovirus serotype providing the chimaeric virus with a desired host range and at least part of a penton or hexon protein from another, less antigenic, serotype. The chimaeric adenoviruses are useful for gene therapy, especially where repeated delivery is required. Adenoviruses of the
                                                                                                                  invention are useful can be constructed to have a desired host range and a diminished capability to raise neutralizing antibodies, an absence of, or decreased infection of, antigen presenting cells of the immune system (e.g. macrophages), and an ability to escape trapping in the liver through increased target cell specificity.
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 7; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                     New chimaeric adenoviruses containing a genome derived from different adenovirus serotypes, useful in gene therapy .
                                                                                                                                                                                                                                                                                                                                                                                                                 HPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INTR-) INTROGENE BV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid
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                                      87.5%;
83.3%;
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                          Score 35; DB 21;
Pred. No. 1.1e+02;
1; Mismatches 0
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                                                   Length 391;
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RESULT 15
Y17401
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Y17400
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Matches
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                                                                                                                                                                                                                                                                                                       The present sequence represents benzylalcohol acetyl transferase (BEAT) from Clarkia breweri plants. BEAT products can be used for producing plants with altered flavour and fragrance characteristics. BEAT nucleic acids can be used for increasing the synthesis of benzylacetate in a plant or for decreasing the benzylalcohol acetate content of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clarkia breweri; Clarkia concinna; benzylalcohol acetyl transferase; BEAT; biosynthesis; acetyl transfer; acetyl CoA; benzylacetate; scen flavour; fragrance.
Clarkia concinna
                            Clarkia breweri; Clarkia concinna; benzylalcohol acetyl transferase; BEAT; blosynthesis; acetyl transfer; acetyl COA; benzylacetate; scent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clarkia
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                                                                                                                         Y17401 standard;
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                                                            Clarkia concinna benzylalcohol acetyl transferase
                                                                                 22-JUL-1999
                                                                                                      Y17401;
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                 cells.
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                                                                                                                                                                                                                                                                                                                                                                                           New isolated benzylalcohol acetyl transferase
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365 nfgwgk 370
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                                                                                                                          Protein; 438
                                                                                                                                                                                                                                 87.5%;
                                                                                                                                                                                                                                Score 35;
Pred. No.
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                                                                                                                                                                                                                        Mismatches
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1.2e+02;
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Search completed: October 20, 2000, 01:35:34 Job time: 142 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 87.5%; Score 35; DB 20; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a benzylalcohol acetyl transferase (BEAT) related protein from Clarkia concinna plants. BEAT products can be used for producing plants with altered flavour and fragrance characteristics. BEAT nucleic acids can be used for increasing the synthesis of benzylacetate in a plant or for decreasing the benzylalcohol acetate content of plant cells.
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N-PSDB; X56426.
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| 374 dfgwg 378
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us-08-894-356c-22.rng

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: October 20, 2000, 03:16:45; search time 151.87 Seconds (without alignments)	Title: US-08-894-356C-22 Perfect score: 17 Sequence: 1 GAYTTYGGNTGGGGNAA 17	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 480022 seqs, 187831343 residues	Total number of hits satisfying chosen parameters:		Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	N_Geneseq_36:* SiDS6/gcgdata/geneseq/geneseqn/NA1980.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1981.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1991.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1991.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1991.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1992.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1992.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1992.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1992.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1992.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1992.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1992.DAT:* SiDS6/gcgdata/geneseq/geneseqn/NA1993.DAT:* SiDS	. ;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Degenerate primer	Geranylgeranyl dip	Clone pTOM36. Lyc	PTOM36 cDNA clone.	Nucleotide sequenc	Aromatic acyl tran	Aromatic acyl tran	Aromatic acyl tran	Melon ripening-rel	Anther specific cD	Aromatic acyl tran	Aromatic acyl tran
SUMMARIES	;	at .		A12000	000110	046682	V02801	T37311	T37312	T37313	T89415	054685	T37310	T37309	
	á	: :	17	5	12	14	6	1	12	17	18	15	17	17	
	Query Match Tongth on	Tall de la	17	23	1080	1080	1096	1479	1508	1518	1526	1542	1605	1622	
æ	Query		83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	
	Score		14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	
	Result No.			0	m	4	S	9	7	œ ·	ָס	10	=:	12	

	Aromatic acyl tran	Anther specific de	Tobacco Ant32 qeno	Human gene express	Human gene signatu	Human colon cancer	Streptococcus phen	Human colon cancer	Neisseria meningi	Netsseria menioat	The state of the s	Clarkia Diewer! De	CTATATA CONCINNA D	Clarkia concinna b	Clarkia concinna b	Streptococcus pneu	Human brain Expres	Cellulase activity	Boyine endothelial	Endothelial nitrog	Xylanase activity	Xylanase activity	Plant microsatell	Nucleotide sequenc	Human secreted pro	EST clone A2285	H. pylori GHPO 111	Human gamma 3 heav	•	Nincleof 140 communication	The section of			Nucleatide express	Duanhas anthonion
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17	15	15	200	2 4		ή α	2.5	; ;	7 6	200	?	20	50	20	10	::	1 -	7 -	1	9 5	7 -	7 7	77.0	2 0	3 6	9 0	, r	1 .	7	20	19	20	20	20	
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83.5	83.5	83.5	77.6	77.6	77.6	77.6	77.6	77.6	77.6	77.6	1 .	9.77	9.//	77.6	77.6	76.5	76.5	76.5	76.5	74.5	74 1	74.1	74 1	74.1	74.1	74 1	74 1	74.1		σ,	7.4.7	4	74.1	74.1	
14.2	14.2	14.2	13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.2		7.0	13.6	13.2	13.2	13	13	13	13	12.6	12.6			12.6	ď	ď	12.6	~			٠,	٠.	∹.	12.6	
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ALIGNMENTS

RESULT

	T37314 standard; DNA; 17 BP.		997 (first entry)	Degenerate primer for identifying aromatic acyl transferase secuence	Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone: colouration; colour	triflora; Petunia hybrida; Perilla ocimoides; cruentus; Lavandula angustifolia; ss.		Location/Qualifiers ure 9	/*tag= a /mod_base I IF 15	•	A1.	96.	16; 96WО-JP00348.	6; 96JP-0046534. 5; 95JP-0067159. 5; 95JP-0196915.	
314	T37314 standard;	T37314;	06-FEB-1997 (fi	Degenerate prime	Aromatic acyl trans plants; acylation;	Gentlana triflora; Scenecio cruentus;	Synthetic.	Key misc_feature	misc_feature]		WO9625500-A1.	22-AUG-1996.	16-FEB-1996; 96	30-JAN-1996; 96 17-FEB-1995; 95 29-JUN-1995; 95	
T37314	O X	AC X	ξΩX	DE XX	KW	X X X	SOX	FF	ra Ta	F F X	N X	. P.	P.Y.	PR PR	44

Gaps

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Indels

Length 23;

DB 21; ;; ;;

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The present sequence represents a PCR primer for a geranylgeranyl diphosphate (GGPP) synthase protein. GGPP synthase has cytostatic activity. A vector encoding GGPP synthase is useful in increasing GGPP synthase levels in a host cell preferably Taxus (Yew) cell and thereby facilitates production, isolation and purification of larger amounts of GGPP synthase in plants. GGPP synthase is useful in obtaining expression or enhanced expression of GGPP and other diterpenes, such as pacilitaxel, useful as anticancer drugs. Isolated nucleic acids encoding gGGPP synthase on hybridising with GGPP synthase encoding nucleic acids
                                                                                                                                                                                                 microorganisms such as Taxomyces andreanae and Penicillium raistrickii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA constructs contg. DNA from pTOM36 clone - used to transform plants to regulate prodn. of the fruit-ripening pTOM36 enzyme
                                                                                                                                                                                 are used for identifying genes encoding GGPP synthase from
                                                                                                                                                                                                                                        Sequence 23 BP; 6 A; 9 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                  83.5%; Score 14.2; I
76.5%; Pred. No. 30;
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76.5%;
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Best Local Similarity 76.5
Matches 13; Conservative
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20 GATTTCGGCTGGGGTAA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geranylgeranyl diphosphate synthase; GGPP synthase; yew; cytostatic; anticancer; Taxus; diterpene; paclitaxel; identification; plant; Taxomyces andreanae; Penicillium raistrickii; microorganism;
                                                                                                                                                                                                                                                        Vectors containing DNA fragments encoding proteins of plant origin
with aromatic acyl transferase activity may be used to transform
plants which produce anthocyanin pigments. The aromatic acyl
transferase acylates the pigments in the flower resulting in colour
                                                                                                                                         plants
                                                                                                                                                                                                                                                                                                                                     tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in 137308-1737313. This degenerate primer was synthesised base on a peptide fragment (W04728) isolated from three of the six clones. It was used to identify other aromatic acyl transferase encoding clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17;
                                                                                                                                       coding for aromatic acyl transferase - for transforming
                                                                                                                                                             produce anthocyanin pigments and thus altering colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geranylgeranyl diphosphate synthase PCR primer SEQ ID NO:6.
                                          Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                          Kusumi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB
Pred. No. 29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 3 A; 0 C; 7 G; 3 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                      ľ, Fujiwara H, Fukui Y,
Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Column 39; 57pp; English.
                                                                                                                                                                                                                      Claim 3; Page 82; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.5%; (
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0187050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0187050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gayttyggntggggnaa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 83.5
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A13989 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Croteau RB, Hefner JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-282526/24.
  (SUNR ) SUNTORY LID.
                                                                                                WPI; 1996-393401/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taxus canadensis,
                                                                                                                                                                             e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6043072-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-2000
                                        Ashikari T,
                                                            Nakao M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A13989;
                                                                                                                                                           which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ~
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                                                                                                                                       DNA
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                                                       This clone is contained in a DNA construct used to transform host plant cells for regulating the prodn. of the enzyme encoded by pTOM36. Plants such as apple, tomato and mango may be modified to produce e.g. sweeter fruit, novel flavour, modified colour or to have improved processing characteristics. The DNA construct pref. also comprises a constitutive or regulatory promoter, e.g. the CaMV 35S or poly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                             Lengt# 1080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                  Sequence 1080 BP; 357 A; 141 C; 207 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 14.2; DB 12;
Pred. No. 44;
2; Mismatches 2;
Disclosure; fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAYTTYGGNTGGGGNAA 17
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Schuch WW

Synthetic.

046682;

RESULT 046682

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Bird CR,

Query Match Best Local Si Matches 13;

V07891;

X 2 X E X E

RESULT V07891

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This is the nucleotide sequence encoding the adenovirus Ad-36p fiber protein used in the method of the invention to determine if a person is suffering viral obesity. The method is used to determine whether obesity in a person has a viral basis. Ad-36p can be used as a basis of a vaccine to prevent viral-based obesity.
                                                                                                                                                                                                                                                                                                                                                                              Determining if obesity in a person is caused by Ad-36 virus - and providing the basis for treatment or prevention of obesity-causing, cholesterol reducing adanovirus, using the purified variant, Ad-36p
                                            Adenovirus; Ad-36p fiber protein; viral obesity; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1096 BP; 353 A; 215 C; 227 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= Aromatic acyl transferase.
                                                                                                                                                  /product "Ad-36p fiber protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.2; DB
Pred. No. 44;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T37311 standard; cDNA to mRNA; 1479 BP.
                                                                                                           Location/Qualifiers
1..1096
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Pages 18-19; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 3..1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocimoides (Clone pSAT208).
                                                                                                                                                                                                                                                                                                                         Atkinson RL, Dhurandhar NV;
                                                                                                                                                                                                                                        98WO-US06730
                                                                                                                                                                                                                                                                      97US-0042942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                            (OBET-) OBETECH LLC.
                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-568305/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 13; Conserv
                                                                           Mastadenovirus
                                                                                                                                                                           WO9844946-A1
                                                                                                                                                                                                                                     06-APR-1998;
                                                                                                                                                                                                                                                                  04-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T37311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
T37311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
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                                                                                                                                                                                                   Transgenic fruit production; prodn.; increased solids content;
higher reducing sugar content; tomato; tomatoes; plant cultivation;
improved; paste; soup; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of the CDNA clone pTOM36 which is believed to encode a cytoplasmic protein of approximately 52000 daltons involved in the ripening of tomatces. The clone is 1069 bases long with an open reading frame of 271 codons. DNA homologous to pTOM36 homologous to brown to a construct that inhibits expression of genes with this construct have increased solids content and a higher content of reducing sugars, e.g. glucose and fructose. The fruit may be managoes, peaches, apples, pears, strawberries, bananas, transformed and case to the produced may be managoes, which are useful in the product of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the fiber protein encoded by adenovirus Ad-36p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic fruit with increased solids content - is obtd. by cultivating plants, esp. tomatces, in which expression of genes homologous to pTOM36 is inhibited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14; Length 1080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1080 BP; 356 A; 141 C; 208 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.2; DB
Pred. No. 44;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 26pp; English.
                                                                                              BP.
                                                                                 Q46682 standard; cDNA; 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V07891 standard; cDNA; 1096 BP.
||:||:|| ||||| ||
866 gatttggatggggaaa 882
                                                                                                                                                                                                                                                                                                                                                                                   92GB-0000520.
                                                                                                                                          18-JAN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                        93WO-GB00021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.5%;
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||:||:|| ||||| ||
866 gattttggatgggaaa 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 76.5
hes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Boniwell JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 1993-243227/30.
                                                                                                                                                                        PTOM36 cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                           (ZENE ) ZENECA LID.
                                                                                                                                                                                                                                                                                                                                                    08-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                              10-JAN-1992;
                                                                                                                                                                                                                                                                                         WO9314212-A
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Gaps

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Indels

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Length 1096;

which DNA

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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin planents. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from
                                                                                                                                     DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1508;
                                   Fukui Y, Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizutani, M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                Seguence 1508 BP; 442 A; 294 C; 295 G; 477 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.2; DB 17;
Pred. No. 46;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                different plants are described in T37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukui Y, Kusumi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T37313 standard; cDNA to mRNA; 1518 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lavandula angustifolia (Clone pLAT21).
                                                                                                                                                                                                         Claim 4; Page 69-72; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1..1355
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashikari T, Fujiwara H, Fukui
Nakao M, Tanaka Y, Yonekura K;
                              Ashikari T, Fujiwara H, Fukui
Nakao M, Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                                              83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0046534.
95JP-0067159.
95JP-0196915.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.5
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUNR ) SUNTORY LID.
(SUNR ) SUNTORY LID
                                                                                     WPI; 1996-393401/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-393401/39
                                                                                                         P-PSDB; W04726
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17-FEB-1995;
29-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                         Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourstions to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313.
                                                                                                                                                                                                                                                            plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1479;
                                                                                                                                                                                                                                                         coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour
                                                                                                                                                       Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1479 BP; 420 A; 316 C; 331 G; 411 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= Aromatic acyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T37312 standard; cDNA to mRNA; 1508 BP
                                                                                                                                                                                                                                                                                                                         Claim 4; Page 65-69; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 3..1367
                                                                                                                                                                       Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Senecio cruentus (Clone pCAT8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.5%;
                                              96JP-0046534.
95JP-0067159.
95JP-0196915.
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95JP-0067159.
95JP-0196915.
                96WO-JP00348
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1167 gattttggatggggaa 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Conservative
                                                                                                                                                                                                         WPI; 1996-393401/39.
                                                                                                                     (SUNR ) SUNTORY LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                            e.g. of flowers
                                                                                                                                                                                                                       P-PSDB; W04725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
                16-FEB-1996;
                                                 30-JAN-1996;
                                                                                   29-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9625500-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-1996;
                                                                 17-FEB-1995
                                                                                                                                                     Ashikari T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1996
                                                                                                                                                                       Nakao M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T37312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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RESULT

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ACCONTRACTOR ACCON

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Gaps

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                                                                   Vectors containing DNA fragments encoding proteins of plant origin plants which produce anthocyanin pigments. The aromatic acyl transferase activity may be used to transform transferase acylates the pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour specific DNA sequences encoding aromatic acyl transferase from sequence is supposed to cross reference with the protein described polypeptide decoded from this sequence and the polypeptide given in the specification and described in W04727, however there are so many discrepancies between the the specification and described in W04727 that the indexer decided
                                                                                                                                                                                                                                                                                                                  Gaps
coding for aromatic acyl transferase - for transforming plants ch produce anthocyanin pigments and thus altering colour tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag* a /note* "contains a putative polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA related with fruit ripening - can be used to genetically modify especially melons to control ripening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This cDNA sequence is from the MEL2 clone which produces a novel ripening-related product from Cucumis melo. It is one of two specified sequences (MEL2) 1526 bp or (MEL7) 686 bp which were
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                      Length 1518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melon cultivar Canteloupe charentals; fruit ripening control; ethylene; MEL2 promoter; ss.
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                 Sequence 1518 BP; 384 A; 340 C; 366 G; 428 T; 0 other;
                                                                                                                                                                                                                                                                                  DB 17;
                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                               Score 14.2; DP
Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Karvouni 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melon ripening-related cDNA clone MEL2.
                                              Claim 4; Page 73-76; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Pages 18-19; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   John I,
                                                                                                                                                                                                                                                                                                        ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                             83.58;
76.58;
                                                                                                                                                                                                                                                                                                                                                                                                          T89415 standard; cDNA; 1526
                                                                                                                                                                                                                                                                                                                                      97WO-GB00824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96GB-0006906
                                                                                                                                                                                                                                                                                                                        1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1385..1526
                                                                                                                                                                                                                                                                                 Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greterson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-503108/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZENE ) ZENECA LTD.
                          e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cucumis melo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09737023-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-1997
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aggelis A,
               which
                                                                                                                                                                                                                                                                                                                                                                                                                                   T89415;
                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
3'UTR
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isolated from a melon ripe fruit cDNA library. MEL2 is not a full-length clone; it lacks the initiation codon for the amino terminus. The cDNA allows control of the ripening of fruit, especially melons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anther specific CDNA or genomic sequences can be used to identify and isolate anther specific promoters. The anther specific promoters can then be cloned into a recombinant construct and used to express the derologous genes. Preferred heterologous genes include Diptheria chryanthemi: T-urfil from cms-T maize mitochondrial genomes; the chryanthemi: T-urfil from cms-T maize mitochondrial genomes; the ciny machine gene from page Mu; the indole acetic acid-lysine from Bacillus thuringlensis Israeliensis. All of these genes when construct can anther tissue will result in the inability of the plant to produce viable pollen. Transformation of plants with such construct can produce transgenic, male sterile plants. Consents self pollination which hinders breeding and hybrid seeds as it
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                               Transgenic plants; male sterility; pollen; sterile; self-pollination; seed; hybrid; toxin-A; peIE; T-urfl3; Gin; iaal; CytA; toxin; Nicotiana tabacum; Diptheria; Erwinia chrysanthemi; phage Mu; Psuedomonas syringae; Bacillus thuringiensis; anther;
                                                                                                                                            ö
                                                                                                                 Length 1526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anther-specific cDNA, genomic and recombinant DNA - produce transgenic male-sterile plants, which prevents self-pollination,
                                                       Sequence 1526 BP; 439 A; 297 C; 331 G; 448 T; 2 U; 9 other;
                                                                                                                                         Indels
                                                                                                              DB 18;
                                                                                                                                         ;
                                                                                                        Score 14.2; DE
Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      Anther specific cDNA clone ant32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 21-24; 75pp; English.
                                                                                                                                                                                                                                                  054685 standard; cDNA; 1542 BP.
                                                                                                        83.5%;
                                                                                                                                                                    93EP-0810455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0908242.
                                                                                                                                                                                                                                                                                                         06-JUL-1994 (first entry)
                                                                                                                Local Similarity 75.5
hes 13; Conservative
                                                                                                                                                       1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66..1412
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crossland LD, Tuttle AB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-010428/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R47475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP578611-A.
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                 954685;
                                                                                                                                                                                                                           10
                                                                                                                             Matches
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Q54685
    88888
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RESULT 11

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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313.
                                                                                                                                                                                                                                                                                          Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= Aromatic acyl transferase.
701..703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.2; DB 17;
Pred. No. 46;
2; Mismatches 2;
   2;
                                                                                                                                                                                                                                                                                                                                                                                Gentiana triflora var. japonica (Clone pGAT106)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_except= AAT encodes Asp
                                                                                                                                                                                                                                                                                                                                              Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encodes
     Mismatches
                                                                                                                                                                                                                                                          Aromatic acyl transferase coding sequence.
                                                                                                                                                      T37309 standard; cDNA to mRNA; 1622 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ', Fujiwara H, Fukui Y,
Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_except=
1322..1324
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95JP-0067159.
95JP-0196915.
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Best Local Similarity 76.5%;
Matches 13; Conservative
                                                       ||:||:|| ||||| ||
|1234 gattttggatggggaaa 1250
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                                                                                                                                                                                                                          (first entry)
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                                   1 GAYTTYGGNTGGGGNAA 17
   13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashikari T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakao M,
                                                                                                                      RESULT 12
T37309
   Matches
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CDS
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                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plants
                                                                                                                                                                                                                                                                                                                                                                                                              Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                    ö
                                                                                    Length 1542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17; Length 1605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
Tanaka Y, Yonekura K;
                                                                                                                      Indels
                                 Sequence 1542 BP; 473 A; 293 C; 332 G; 444 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1605 BP; 477 A; 319 C; 375 G; 434 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
67.1413
/*tag= a
/product= Aromatic acyl transferase.
                                                                                    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             different plants are described in T37308-T37313.
                                                                                  Score 14.2; D
Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.2; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                              Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                        T37310 standard; cDNA to mRNA; 1605 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 61-65; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petunia hybrida (Clone pPAT48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96JP-0046534.
95JP-0067159.
95JP-0196915.
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76.58;
                                                                                  83.5%;
76.5%;
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|1239 gattttgggttggggaaa 1255
                                                                                                                                                                                                                                                                                                                                          06-FEB-1997 (first entry)
                                                                                                                                                    1 GAYTTYGGNTGGGGNAA 17
                                                                                  Query Match 83.5
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUNR ) SUNTORY LTD.
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P-PSDB; W04724.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-1996
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production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashikari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakao M,
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Key

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Gaps

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plants tone,

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Transgenic plants; male sterility; pollen; sterile; self-pollination; seed; hybrid; toxin-A; peIE; T-urfl3; Gin; iaal.; CytA; toxin; Nicotiana tabacum; Diptheria; Erwinia chrysanthemi; phage Mu; Psuedomonas syringae; Bacillus thuringlensis; anther; breeding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anther-specific cDNA, genomic and recombinant DNA - produce transgenic male-sterile plants, which prevents self-pollination,
                                                                             Anther specific genomic clone ant32.
            Q54693 standard; DNA; 3706 BP.
                                                       06-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                            (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in hybrid seed prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-010428/02.
                                                                                                                                                                    Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R47475
                                                                                                                                                                                                                                                                                                                                                                                                   Crossland LD,
                                                                                                                                                                                        Key
TATA_signal
                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                   24 - JUN - 1993;
                                                                                                                                                                                                                                                                                                                                                        02-JUL-1992;
                                                                                                                                                                                                                                                                                                             12-JAN-1994
                                                                                                                                                                                                                                                                                       EP578611-A.
  054693
                        Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA coding for aromatic acyl transferase – for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                              Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 1703;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukui Y, Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1703 BP; 512 A; 353 C; 356 G; 482 T; 0 other;
                                                                                                                                                                                                                                           Location/Qualifiers
6..1415
/*tag- a
/Product- Aromatic acyl transferase.
                                                                                                                                                                                                                    Gentiana triflora var. japonica (Clone pGAT4).
                                                                                                                                         Aromatic acyl transferase coding sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.5%; Score 14.2; D
76.5%; Pred. No. 46;
tive 2; Mismatches
                                                                         T37308 standard; cDNA to mRNA; 1703 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 53-57; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                               ?, Fujiwara H, Fukui
Tanaka Y, Yonekura K;
            1277 gattttggttggggaaa 1293
                                                                                                                                                                                                                                                                                                                                                               96JP-0046534.
95JP-0067159.
95JP-0196915.
                                                                                                                                                                                                                                                                                                                                            96WO-JP00348
                                                                                                                   06-FEB-1997 (first entry)
 1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 76.5'
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (SUNR ) SUNTORY LTD.
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                                                                                                                                                                                                                                                                                                WO9625500-A1.
                                                                                                                                                                                                                                                                                                                                         16-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Ashikari T,
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                                                                                                T37308;
                                                     RESULT 13
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/*tag= c /note= "Putative transcription start site."

93EP-0810455. 92US-0908242.

Tuttle AB:

Location/Qualifiers 1971..1975 /*tag- a 2076..3422 /*tag- b

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                                                 Anther specific cDNA or genomic sequences can be used to identify and isolate anther specific promoters. The anther specific promoters can then be cloned into a recombinant construct and used to express the terologous genes. Preferred heterologous genes include Diptheria chrysathemi: T-urfl3 from cms-T maize mitochondrial genomes; the cirysathemi: T-urfl3 from cms-T maize mitochondrial genomes; the cirysathemi: T-urfl3 from pseudomonas syringae and the Cyta toxin gene synthetase gene from pseudomonas syringae and the Cyta toxin gene cypressed in anther tissue will result in the inability of the cyprate to produce viable pollen. Transformation of plants with such male sterility is important in the production of plants with such male sterility is important in the production of hybrid seeds as it condiments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3706 BP; 1097 A; 668 C; 696 G; 1245 T; 0 other;
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Pred. No. 50;
2; Mismatches
Claim 4; Page 48-54; 75pp; English.
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RESULT

1 GAYTTYGGNTGGGGNAA 17

Job time: 5994 sec

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Dual method for producing male-sterile plants – comprises crossing 2 genetically transformed plants, useful for producing hybrid seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q58340 is an anther specific clone from Nicotiana tabacum. The ant32 promoter can be operably linked to, eg. T7 RNA polymerase gene or to GAL4/VPI fusion gene in order to produce male-sterile plants. The inventors claim that male-sterile plants finally produced can be used to increase hybrid vigour in plants, e.g. maize.
                                                                                                                                                                                                              /*tag= b
/note= "putative transcription start site"
/*tag= c
/note= "ant32 promoter can be obtained from
the 2.0kb 5' flanking region of the
ant32 clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3706 BP; 1097 A; 653 C; 709 G; 1247 T; 0 other;
                                                                                                            ant32 promoter; genomic clone; male-sterile plants; fusion genes; ss.
                                                                                                                                                                  Location/Qualifiers
1971..1975
/*tag= a
2009
                                                                                        Tobacco Ant32 genomic clone sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 22-28; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Crossland LD, Stein JI, Tuttle A;
                      Q58340 standard; DNA; 3706 BP.
                                                                                                                                                                                                                                                                                                                                                                       93EP-0810654
                                                                                                                                                                                                                                                                                                                                                                                           92US-0950348
                                                                                                                                                                                                                                                                                         2076..3422
/*tag= d
                                                                  27-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-119827/15.
P-PSDB; R46929.
                                                                                                                                              Nicotiana tabacum.
                                                                                                                                                                                                    misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-1992;
                                                                                                                                                                                TATA_signal
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                                            058340;
RESULT 15
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Score 14.2; DB 15; Length 3706; Pred. No. 50; 2; Mismatches 2; Indels 0;

Query Match
Best Local Similarity 76.5%;
Matches 13; Conservative

1 GAYTTYGGNTGGGGNAA 17

Search completed: October 20, 2000, 03:16:47

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Result
No.
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

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/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/FCTOMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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  GenCore version (c) 1993 - 2000
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US-09-7-598-873-1
US-08-37-598-873-1
US-08-396-531-1
US-08-396-531-1
US-08-207-904-16
US-08-207-904-16
US-08-208-245-1
US-08-646-590B-24
US-08-646-590B-24
US-08-696-182A-1
US-08-696-182A-1
US-08-696-182A-1
US-08-786-198-780-1
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PCTT-US-08-780-1
US-07-695-472B-36
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24.849 Million cell updates/sec
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19, 19,	Sequence 89, App. Sequence 89, App. Sequence 30, App. Sequence 30, App. Sequence 5, App1.	15 1, 1, 1,	Sequence 4, Appl1 Sequence 35, Appl Sequence 59, Appl1 Sequence 1, Appl1 Sequence 5, Appl1

ALIGNMENTS

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Sequence 6, Application US/09187050B

Patent No. 6043072

GENERAL INPORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Hefner, Jerry

TITLE OF INVENTION: Synthase, And Methods of Use

FILE REFERENCE: WSUR12423

CURRENT APPLICATION UNUMBER: US/09/187,050B

CURRENT APPLICATION UNUMBER: US/09/187,050B

CURRENT APPLICATION UNUMBER: US/09/187,050B

CURRENT FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 23

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:

CHUER INCORPATION. Description of Artificial Security
Sequence 1, Application US/07598873 Patent No. 5254800
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_difference
LOCATION: (1)..(23)
OTHER INFORMATION: No. 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                           20 GATTTCGGCTGGGGTAA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description of Artificial Sequence: non-degenerate reverse PCR primer
                                                                                                                                                                                                                                                                                                                                            83.5%;
                                                CONSTRUCTS, CELLS AND PLANTS
                                                                                                                                                                                                                                                                                                                            Score 14.2; DB Pred. No. 5.7; 2; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L Street, N.W.

Washington

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, OKGANISM: Lycopersicon esculentum; STRAIN: Ailsa Craig; DEVELOPMENTAL STAGE: Ripening US-07-598-873-1
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                        COUNTRY: USA
ZIP: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: BIRD, CO
APPLICANT: BONIWEL
APPLICANT: GRIERSO
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INFORMATION FOR SEQ ID NO: 1:
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STRANDEDNESS: double
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: CUSHMAN, DARBY & CUSHMAN
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                          APPLICANT: RAY, JOHN A
APPLICANT: SCHUCH, WOLFGANG W
TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 866 GATTTTGGATGGGGAAA 882
                                                                                                                                                                                         STREET: 1100 New CITY: WASHINGTON
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                 APPLICATION NUMBER:
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Similarity 76.5%;
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                   US/08/073,425
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Best Local S
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                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,037
ETLING DATE: 16-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
            TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/396,531
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: RAY, JOHN A
APPLICANT: SCHUCH, WOLFGANG W
TITLE OF INVENTION: DAY, CONSTRUCTS, C
TITLE OF INVENTION: DERIVED THEREFROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: cD
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LENGTH: 1080 base pairs
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 23,04 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: DEAVER, DONALD B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          866 GATTTTGGATGGGGAAA 882
                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Lycopersicon esculentum STRAIN: Ailsa Craig DEVELOPMENTAL STAGE: Ripening
                                                 TELEPHONE: 202-861-300
TELEFAX: 202-822-0944
                                                                                                                                                                                                          FILING DATE: CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202-861-30
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                     20005-3918
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Ninth Floor, 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                     USA
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Pred. No. 10;
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nucleic acid

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; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum
; STRAIN: Ailsa Craig
; DEVELOPMENTAL STAGE: Ripening
US-08-396-531-1
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APPLICANN: John, Isaac
APPLICANT: KATVOUNI, ZO1
TITLE OF INVENTION: Fruit Ripening
FILE REFERENCE: SEESOIL/UST
CURRENT APPLICATION NUMBER: US/09/142,514A
CURRENT FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: PCT/GB97/00824
EARLIER FILING DATE: 1997-03-24
EARLIER APPLICATION NUMBER: GB 9606906.7
EARLIER APPLICATION NUMBER: GB 9606906.7
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; TYPE: DNA
; ORGANISM: Cucumis melo
US-09-142-514-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                            Sequence 1, Application US/08207904 Patent No. 5477002
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Best Local :
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Best Local Similarity
                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aggelis, Alexandros APPLICANT: Grierson, Donald
                                                                                       APPLICANT: Tuttle, AnnMarie
APPLICANT: Crossland, Lyle D.
TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
                                                                                                                                                                                                                                                                                           1122 gactttggatgggaaa 1138
                                                                             CORRESPONDENCE ADDRESS:
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                            STREET: 7 Skyll CITY: Hawthorne
                                 ADDRESSEE: Clam CL.
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COUNTRY:
                STATE:
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               New York
   USA
                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                              CIBA-GEIGY Corporation
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76.5%;
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76.5%;
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Pred. No. 11;
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; LOCATION:
US-08-207-904-1
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Best Local Similarity
Matches 13; Conserv
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Patent No. 5477002
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1239 GATTTTGGGTGGGGAAA 1255
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ORIGINAL SOURCE:
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LENGTH: 1542 base pairs
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tuttle, AnnMarie APPLICANT: Crossland, Lyle D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: N
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                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                  STREET: 7 Skylin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/908,242
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OPERATING SYSTEM: PC-DOS/MS-DOS
                   CLASSIFICATION: 800
                                                                                                                                                                                                                          ADDRESSEE: Clbm-cur-
cmpreff: 7 Skyline Drive
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                                                                                                                                                                                                      New York
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76.5%;
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                                                  US/08/207,904
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Pred. No. 11;
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Gaps

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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER:

US/07/908,242

REFERENCE/DOCKET NUMBER: CG

CGC 1624

NAME: Lazar, Steven R. REGISTRATION NUMBER: 3

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OTHER INFORMATION: /note= "putative transcription other information: start site"
US-08-207-904-16
                                                                                                                                                                                                                                                                                                                                                                           US-07-908-245-1/c

: Sequence 1, Application US/07908245

: Patent No. 5498539
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                                                      CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PS-DOS PERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Harrison, David G.
APPLICANT: Alexander, R. Wayne
APPLICANT: Murphy, T.J.
APPLICANT: Nishida, Ken'ichi
TITLE OF INVENTION: Endothelial Nitric Oxide Synthase
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NAME/KEY:
LOCATION:
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,245
FILING DATE: 19920702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3249 GATTTTGGGTGGGGAAA 3265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Nicotiana tabacum INDIVIDUAL ISOLATE: Ant32 genomic clone IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8615
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                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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LOCATION:
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nes 13; Conserv
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                                                                                                                                                                                                       1100 Peachtree Street, Suite 2800
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2076..3422
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76.5%;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3706;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 74, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 1:
                          TELECOMMUNICATION INFORMATION: TELEPHONE: (517) 636-8104
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3840 GACTTAGGGTGGGGAAA 3824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: BOY!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
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LENGTH: 4089 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                               ZIP:
                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                        STREET: P.O. BOX 1967
CITY: MIDLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL TYPE: Endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE:
                                                                                                                   FILING DATE:
                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                             48641-1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1, Application US/08822028
5993813
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                                                                                                                                                                                                                                                                                                                           MICHIGAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOURLIE, BRIAN B
RIXON, MARK W
                                                                                                                                                                                                                                                                                                                                                                                                          SCHOLOM, JEFFREY
VENTION: A NOVEL FAMILY OF HIGH AFFINITY,
VENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEZES, PETER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAPLAN, DONALD A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANDERSON, WH KERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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E: Aorta
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                                                                     34,941
                                                        C-37,075C
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Pred. No.
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65;
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; LENGTH: 508 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-822-028-74
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RESULT 11
US-08-646-590B-24
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:

OLD UO.

ACTERISTICS:

1912 NUCLEOTIDES

STRANDEDNESS:

TOPOLOGY:

OLD UO.

OLD UO
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STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 331
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,171A
FILING DATE: Concurrently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: HERRON, CHARLES J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                            1 GAYTTYGGNTGGGGNAA 17
||:||:|| || || || ||
686 GACTTCGGGTGGAGGAA 702
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||:||:|| ||||| |
25 GACTTTGGCTGGGGGCA 41
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FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                Match 74.18;
Local Similarity 70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
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12; Conserv
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                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.18;
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Pred. No. 80;
2; Mismatches
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                                                                                                                                                                                                                                                                                                Score 12.6;
Pred. No. 8
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                      88;
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                                                                                                                                                                                                                                                                                                                           Length 912;
                                                                                                                                                                                                                                                                Indels
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                                                                                                                  Sequence 24, Application US/09069226
Patent No. 6013509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 912 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                    Query Match
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NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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PRIOR APPLICATION DATA:
08/599,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97.
FILING DATE: 21-January-1997
CLASSIFICATION: 435
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Warren, Patrick V.
APPLICANT: Swanson, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Warren, F
                                                                   APPLICANT: WARREN, Patrick V.
TITLE OF INVENTION: TRANSAMIN
NUMBER OF SEQUENCES: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                    CORRESPONDENCE ADDRESS:
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              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01 FILING DATE: 08-May-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                   Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11
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ZIP: 92037
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STREET:
                                                                                                                                                                                                                                                                                1 GAYTTYGGNTGGGGNAA 17
 6 BECKER FARM ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
E: Genomic DNA
                    CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                   74.1%;
                                                                      TRANSAMINASES AND AMINOTRANSFERASES 32
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                   Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC

IBM PS/2

INCH DISKETTE

COUNTRY:

USA

07068

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US-08-096-182A-1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO:
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             APPLICANT: Q1, Huilin L.
APPLICANT: Liang, Shu-Mei
APPLICANT: Liang, Shu-Mei
APPLICANT: Hronowski, Lucjan J.J.
APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for the High Level Expression,
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 33:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 912 NUCLEOTIDES
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Blake, Milan S. APPLICANT: Tai, Joseph Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: GENOMIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686 GACTTCGGGTGGAGGAA 702
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             APPLICATION NUMBER: US/08/096,182A FILING DATE: 23-JUL-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 70.0 es 12; Conservative
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STRANDEDNESS: SINGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/069,226 FILING DATE:
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                                                                                                                                                                                                                                                                       E: Sterne, Kessler, Goldstein & Fox 1100 New York Ave., Suite 600
                                                                                                                                                                                                             USA
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Qi, Huilin L.
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Pred. No. 88;
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RESULT 14
US-08-877-109-1
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; LOCATION:
US-08-096-182A-1
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                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,26
FILING DATE: 28-APR-1995
APPLICATION NUMBER: 08/096,18
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
                   TELEFAX: (202) 371-25.
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hronowski, Lucjan J.J.
APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for the High Level Expression,
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group
TITLE OF INVENTION: Porin Proteins from Neisseria meningitidis
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                                                  REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 930 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
SEQUENCE CHARACTERISTICS:
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nes 12; Conserv
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                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
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                                    (202) 371-2540
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Hronowski, Lucjan J.J.
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Qi, Huilin L.
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70.6%;
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                                                                                          1438.0060001
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Pred. No. 88
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APPLICANT: Tal, Joseph Y.
APPLICANT: Tal, Joseph Y.
APPLICANT: 1140 J. Hullin L.
APPLICANT: Liang, Shu-Mei
APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
UNUMBER OF SEQUENCES: 23
CORRESSONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox
CITEET: 1100 New York Ave., Suite 600
STATE: D.C.
COUNTRY: USA
COMPUTER READRABLE FORM:
KEDIUM TYPE: Ploppy disk
OPERATINA SYSTEM: PC-DOS/MS-OOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US./08/798,760
TILING DATE: 11-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ARE SETENCE/DOCKET NUMBER: 1438.0060002
TELEPHONE: (202) 371-2500
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 930 base pairs
TPE: nucleic acid
STRANDEDNESS: double
FEATURE: Deth
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                                                                                                                                FEATURE:

NAME/KEY: CDS
LOCATION: 1.930
US-08-798-760-1
                                            Query Match 74.1%;
Best Local Similarity 70.6%;
Matches 12; Conservative
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US-08-798-760-1
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US-08-877-109-1
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Patent No. 6013267
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Best Local Similarity 70.6
Matches 12; Conservative
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APPLICANT: Blake,
APPLICANT: Tai, Jo
1 GAYTTYGGNTGGGGNAA 17
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196 GACTCCGGTTGGGGCAA 212
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70.68;
                                          Score 12.6; Di
Pred. No. 88;
2; Mismatches
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; Pred. No. 88;
2; Mismatches
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Db 196 GACTCCGGTTGGGGCAA 212

Search completed: October 20, 2000, 03:12:36 Job time: 5774 sec

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Title:
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1: 9b
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length: 2000000000
      Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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58.628 Million cell updates/sec
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A0034368 C1T-HSP-2

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R63685 y110f04.s1

A1967062 496021B11

AU096989 AV407679

BE213479 GF-Fy-P6E

BE020415 sm43h12.y

AV439490 AV4025743

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AW3186527 sb54c08.y

AV425743

W08160 mb42d05.r1

AW318655 un03b01.y

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A1899217 EST268660

AW255739 ML800 Pep

AW650751 EST398596

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 314 400 1010
Email: estewatson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40RP from Gibco
High quality sequence stop: 212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,G.
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Sybean EST Project
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AI494813.1 GI:4395816
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//note-wector: pBluescript II XR; Site_1: EcoRI; Site_2: AhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used [GAGAGAGAGAGAGAGAGAGAGAGAGTG-18]. After second-strand synthesis, the cDNA were 'pollshed' with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with xhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, Az 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu, 168 t
       52
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/clone="GENOW"
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/lab_host="XL10-Gold"
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Gm-c1004-7183

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-322: FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108,
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/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizoblum Japonicus, strain USDA10 priot to harvest. Strategene's cDNA synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="GENOME SYSTEMS CLONE ID: Gm-c1028-687"
/clone_lib="Gm-c1028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Glycine max"
/db_xref="taxon:3847"
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76.5%;
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Pred. No. 7.5e+02;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 247)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Llang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI488429
AI488429.1 GI:4383800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University
100 Jordan Hall, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation of ESTs from tomato carpel tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids i; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: dfrisch@CLEMSON.EDU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.D. and Giovannoni, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                        /lab_host="XL1-Biue MRF'"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="Vector: pBlueScript Sk(-); Site_1: EcoR1; Site_2: EcoR1; Sit
                                      respectively.
                                                                                                              and 3' ends located at the EcoRI and XhoI sites,
                                                                                                                                                                                                                                                                                                            /clone_lib="tomato ovary, TAMU"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon esculentum"
/culrtyar="TA496"
/db_xref="taxon:4081"
/clone="cLED21D13"
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Pred. No. 7.
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Query Match Best Local Similarity

83.5%; 76.5%;

Score 14.2; DB 11; Pred. No. 7.6e+02;

Length 247;

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RESULT
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                                                                                                      1 GAYTTYGGNTGGGGNAA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (linfo@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 258 row: D column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Other_GSSs: RPCI-23-258D7.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 249)
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RPCI-23-258D7
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Mouse BAC End Sequences from Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zhao,S., Nierman,W., Feldblyum,T., Malek,J., Sh,
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence.
AZ015624
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                                                                                                                                        Conservative
                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAC ends.
                                                                                                                                                                                                                                      note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DHIOB electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="RPCI-23-258D7"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                              /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                /sex="Female"
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76.5%;
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F RPCI-23
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RESULT 6
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                                                                                                                                                                                                                            AA651035
31149 Lam
                                                      Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; S
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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Tel: 517-353-0854
Fax: 517-353-9168
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MSU-DOE Plant Research Laboratory
Michigan State University
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                                                                                                                                              EST
                                                                                                                                                                                    AA651035
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EST.
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30868 Lambda-PRL2 Arabidopsis thaliana cDNA clone 281H6T7, mRNA
Newman, T.,
                    Brāssicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 263)
                                                                                                                                                                 AA651035.1
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                                                                                                                         thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: 22313tcn@ibm.cl.msu.
Seq primer: T7 dye primer.
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Lambda-PRL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda RRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated eticlated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and slilques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. "

10 others
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/clone="281H6T7"
/clone_11b="Lambda-PRL2"
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/strain="var columbia"
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  deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh
                                                                                                                                                                 GI:2581127
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76.5%;
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Arabidopsis thaliana cDNA clone 168a5XP
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Pred. No. 7.6e
2; Mismatches
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                                                                                                                                       Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Thelsing,B., Allen,M., Bowers,Y., Pe,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ri,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       vh93f09.x1
cDNA clone
                                                            Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicire
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI608251
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The sequence entry for this EST has been reverse complimented
is being submitted in the sense orientation.
Seq primer: M12_Universal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
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                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                Mus musculus
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Tel: 517-353-0854
Fax: 517-353-9168
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,E. and Somerville,C.
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA siliques.
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/clone="168A5XP"
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/strain="var columbia"
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76.5%;
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                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.2; DB 5;
Pred. No. 7.6e+02;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                               Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, K., Shibata
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamanura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
M., Muramatsu, M. and Hayashizaki, Y.
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:522529
                                                Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westove
                                                                                                                                                                                     3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                 Genome Exploration Research Group, Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carn, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, J., Linkawa, T., Ito Tizawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.
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BB264508 RIKEN full-length enriched, 10 days neonate cortex
musculus cDNA clone A830015G22 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                         The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB264508.1 GI:8960965
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                                                                                                                                                                                                                                                                                                                 Sciences Center
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/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:894569"
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Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Y., Muramatsu,M. and Hayashizaki,Y.
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76.5%;
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Pred. No. 7.7e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Science Tsukuba Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 278;
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                                                     Sasaki
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                                                                                              Glycine max

Glycine max

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;

Budoryota; Viridiplantae; Embryophyta; Tracheophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae

Fabales; Fabaceae; Papilionoldeae; Glycine.

1 (bases 1 to 307)

1 (bases 1 to 307)
                                                                                                                                                                                                                                                                                                                                                                AW471629 307 bp mRNA EST 24-FEB-2000 sil3h01.yl Gm-cl029 Glycine max cDNA clone GENOME SYSTEMS CLONE Gm-cl029-1130 5' similar to TR:004201 004201 HYPERSENSITIVITY-RELATED GENE 201 ISOLOG. ;, mRNA sequence.
                  Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., E Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., E, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki V. and Hayashia, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki V. and Hayashia, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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Carninci,P. and Hayashizaki,Y.

Righ-efficiency full-length cDNA cloning. Methods Enzymol. 303
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Person, B., Swaller, T., Ritter, E., Kohn, S., Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified pBluescript KS(+) after bulk excision from Lambda
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/lab_host="DH10B"
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/clone="A830015G22"
/clone_lib="RIKEN full-length enriched, 10 days neonate
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  Kohn, S., Shin, T.,
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  Jackson,Y.,
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                                                                                                                                                                                  Rosidae;
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Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., I, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., R., Waterston,R., and within the state of the s
                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.

1 (bases 1 to 324)

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI856623
AI856623.1 GI:5510239
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1856623 324 bp mRNA EST 16-JUL-1999 sb39912.yl Gm-c1014 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1014-95 5 similar to TR:004201 004201 HYPERSENSITIVITY-RELATED
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13; Conserv
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: pSPORT1; Site_1: Not I; Site_2: Sal I; This cDNA library was constructed from mRNA isolated from very young cotyledons (20-50mgs fresh weight) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I -Sal I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
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plants"
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/clone_lib="Gm-c1029"
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Pred. No. 7.7e+02;
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Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 33)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                         Homo sapiens
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CIT-HSP-2319K4.TF
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40RP from Gibco
High quality sequence stop: 311.
Location/Qualifiers
1 224
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Other_ESTs: sb39g12.x1
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93 a 49 c 101 g 79 t 2 others
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/db_xref="taxon:3847"
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76.5%;
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CIT-HSP Homo sapiens genomic clone
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Pred. No. 7.7e+02;
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Suh,E., Wible,C., Shizuya,H.,
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                                                                                                                                                                                                                                               Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, U:
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                        Generation of ESTs from tomato fruit tissue,
                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 347)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksle,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sper Magnoliophyta; eudicotyledons; core eudicots; Asteridae; I; Solanales; Solanaceae; Solanum; Lycopersicon.
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ST412000 tomato breaker fruit, clone cLEG31N6, mRNA sequence.
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13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Clones are available from Research Genetics (info@resgen.com). BAC
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Tel: 301 838 0200
Fax: 301 838 0208
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/note-"Vector: pBluescriptSKmCUadapt; Site_1: EcoR];
Site_2: XhoI; Fruit were harvested at the breaker st
(first sign of lycopene accumulation on the blossom
                                                          /clone_lib="tomato breaker
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                        /organism="Lycopersicon
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG31N6"
                                                                                                                                                                                                    Location/Qualifiers
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/db_xref="taxon:9606"
/clone="2319k4"
/clone_lb="CIT-HSP"
/sex="Male"
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a 100 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
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Genoscope - Centre National de Sequencage
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                      mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."

80 g 119 t
                                                                                                                                               nitrogen-rich medium for 21 days. Three days before inoculation with Sinorhizobium meliloti, the medium was replaced by N-free medium. Root nodules (+ short adjacent root segments) were harvested 4 days post inoculation. CDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-systed from there is the containing cDNA inserts were
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type-"symbiotic root nodules"
/dev_stage="harvested 4 days post inoculation with
Sinorhizobium mellioti"
                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
71 c 40 g 116 t
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Query Match

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This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888)919-3324 or (314)
Call: (800) 430-0030 or (314) 427-3222 FAX: (888)919-3324 or (314)
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Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Coryell,V., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and Lewin,H.
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Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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Tel: (217) 244-6147
Fax: (217) 333-4582
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BASE COUNT ORIGIN 밁 Ş TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS FEATURES REFERENCE AUTHORS SOURCE ORGANISM Query Match Best Local S Matches 13 DEFINITION RESULT R63685 밁 ş Locus Best Local Similarity 76.5 Matches 13; Conservative ||:||:|| |||| || 351 GATTTTGGTTGGGGAAA 367 source -330 GACTTTGGTTGGGGGAA 314 15 1 GAYTTYGGNTGGGGNAA 17 GAYTTYGGNTGGGGNAA 17 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; vercental primates; Chordata; Craniata; vercental primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 389)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Wohldmann,P. and Wilson,R. l Similarity 13; Conserv Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: estéwatson.wustl.edu
Insert Size: 828 R63685 389 bp mRNA EST 26-MAY-1995 Y110f04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138847 3' similar to gb:X53743 FIBULIN-1, ISOFORM C PRECURSOR R63685.1 HUMAN);, mRNA sequence. Conservative 89 /db_xref="taxon:9606" /clone="IMAGE:138847" /clone_lib="Soares placenta Nb2HP" /organism="Homo sapiens" /db_xref="GDB:545291" /sex="Female" GI:835564 83.5%; 76.5%; Score 14.2; DB 38; Pred. No. 7.9e+()2; 2; Mismatches 2; Pred. No. 7.8e+02; 2; Mismatches 2; Length 389; Indels Indels 0; 0, Gaps Gaps 0 0

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                                   ataatgccattatatacttccataaagtatcctatgcaatagagaacatgttatgtgtta
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17-FEB-1995;
29-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 69-72; 94pp; Japanese.
                                                                                                                                                                                                                                                         Sequence 1508 BP; 442 A; 294 C; 295 G; 477 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                           DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashikari T, Fujiwara H,
Nakao M, Tanaka Y, Yone)
           178
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P-PSDB; W04726.
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                                                         118
                                                               145 TGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCTTAATCTTA
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                                                                                                                                                           1 tgaacattctcgaacatgcccgaatatcggccccctcgggcacca---tcggccatcgct
AGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGC
                                                                                                cgttatctcttactttcttcgacattacttggctactcttccctccggtccaccatcttt
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                                                 tcttctatgactttccacattctaaatcccatttcatcgacactattgttcccaggctaa
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95JP-0067159.
95JP-0196915.
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/product= Aromatic acyl tra;sferase.
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kura K;
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Pred. No. 1.1e-44;
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1276 CTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCAGGGATTTTGAAAAAAGGTGTGG 1335 	Оy
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GCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAAGTTTTGTAA S	Qy
ttcaagtgacgttttttccgggct 4	DЬ
ACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACC	Οу
8 atcctcgaaaatgtgaaaacttttatccacttgtaccttcattg	Db ·
76 AACTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATCTTTATCCTTACCCCCCTTTTATCCCA	νQ
298 attetgttgtggttacttttgcagaatgttqtctttgctttaataatttgacagaaaac 35	B 3
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                                                                Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T97308-T97313. NOTE: This sequence is supposed to cross reference with the protein described in W04727, however there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide decoded from the specification and described in W04727 that the indexer decided not to cross reference the two.
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                                                                                                                                                                                            Claim 4; Page 73-76; 94pp; Japanese
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Gentiana triflora;
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Tanaka
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acylation; colour; tone; colouration
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naka Y, Yonekura K;
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GATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTATTGGCAACTGTCTTGCG
gctgaggcgatcgcggggaaatagagaagaggacg---
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                                                                                                   tttgcgatggcgaagatcctgcggcgggatttggtcggagatgaaggggtgtttcgggca
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17-FEB-1995;
29-JUN-1995;
                                                         DNA coding for aromatic acyl transferase - which produce anthocyanin pigments and thus e.g. of flowers
                                                                                                                                                                      WPI;
                 Claim 4; Page 57-61;
                                                                                                                                              P-PSDB;
                                                                                                                                                                                                     Ashikari T, Fujiwara H, Fu)
Nakao M, Tanaka Y, Yonekura
                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1996;
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CGTTCACAATGACGTGTGGATACGTATGGACATGGATGGTCAAATCAAAAGATGACGTCG
                                                                                                                CTCGATTCAACAAGGTACGAGCTACATATGTCCTCTCCCTTGCTGAAATCCAGAAGCTAA
                                                                                                                                                                                                                                            ATCTTCCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTATGGCCTAGAGGAAACAT
                                                                                                                                                                                                                                                                                      TCAATGCTTGGGCCTATATTAACAAAT---TTGGGAAAGACGCGGACTTGTTGTCCGCGA
                                         agaaattcatttcgtcaaaaaatcgcaacttaaccggtagtagtaattataatctgtcaa
                                                                                               tttctaaagalgaagttcgagccaccttcatcctacaccctattgatatcatgaagctca
                                                                                                                                                                            TTTGGAACGAAATGCAAGATGT---TCTTGAAATGTTCTCTAGATTTTGGAAGCAAACCCC
                                                                                                                                                                                                                                                                       AG-AACAAAGTACTGAATCTCAGAGGATCCGAACCGACAATA-----CGTGTAACGA
                                                                                                                                                        tctacaatgaaagaaactgctcaaatctcagggcacacctactgttctaaatccagcaa
                                                                                                                                                                                                                cttctctacctatgtacgacagatctgtggtgcaagatccatttcatattcgtcgaaaaa
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                                                                                                                                                                                                                                                                                                                                             TAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTTTGTAATGTTCA
                                                                                                                                                                                                                                                                                                                                                                                      gcgac---gaagtattaccactttttgctttacaggtgacggtgttctccaacaccggta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 A; 354 C; 313 G;
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2.9e-40;
les 620;
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                                                                                                                                                   Perilla ocimoides
                                                                                                                                                                    Scenecio
                                                                                                                                                                          plants; acylation;
Gentiana triflora;
                                                                                                                                                                                            Aromatic acyl transferase; transformation;
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         (SUNR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctttcacggtgacatctgcactgatctggacatgcttgtcgaaatcattagacaccgtcg
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                                                                                                                                                                                                                                                                                                                                                   GGGATTTTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAAGATTCATATGGATGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taagagagaa---ggtggaagaggataaacatgcagcaaacttatgtgctttcatcaact
         SUNTORY
                                                                                                                                                                   cruentus;
                                                                                                                                                                                                            acyl
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                          transferase coding sequence.
                        96JP-0046534.
95JP-0067159.
95JP-0196915.
                                                          96WO-JP00348
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/*tag=
                                                                                                          /product=
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                                                                                                                                                  (Clone pSAT208).
                                                                                                                                                                          colour; tone; colouration; colour of Petunia hybrida; Perilla ocimoides
                                                                                                                                                                  Lavandula angustifolia;
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                                                                                                                                                                                                                                                             mRNA;
                                                                                                         Aromatic acyl transferase.
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DNA coding for aromatic acyl transferase - which produce anthocyanin pigments and thus e.g. of flowers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashikari T, Fujiwara H, Fuk
Nakao M, Tanaka Y, Yonekura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAG
                                                                                                                                                                                                         GCGAATCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTATGGCCCTAGAGGAA
                                                                                                                                                                                                                                                                                                                              TTCATCAATGCTTGGGCCTATATTAACAAA---TTTGGGAAAGACGCGGACTTGTTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       teggtttettteaceategeagaatetagegaegaettegatgatetegteggaaategt 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGATGCCGATCAAATCGGGCGAAATGCCGGAGTTTCAGTACTCCCGTGATGAGGGCGAC 317
CCTCGATTCAACAAGGTACGAGCTACATATGTCCTCTCCCTTGCTGAAATCCAGAAGCTA
                                                                                        ACATTTTGGAACGAAATGCAAGATGTTCTTGAAATGTTCTCTAGATTTTGGAAGCAAACCC
                                                                                                                                                                                                                                                                                            tttataacggcttggtcttcaatgagcaaacacattgaaaatgaagatgaagaa
                                                                                                                                                                                                                                                                                                                                                                                                                ggcgtcggtattggaatagcaacgcatcacaccgttagcgacgccccgtcgtttctcgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTTGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---tccgatagaaaactcttccaagttttcgccgtgcaggtgactcttttcccaggccga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atctacccttcatcccggagaaaatgccggagtttcggta----tctatccggggac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cageteetettetaegaatteeettgtteeaageaacattttteagaateeategtteea
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                                                       atttattggagaaacgcgctaaaatttcct-----ttgcaatctcgtcatccctca
                                                                                                                                                                           tttaaatctttgccagttttcgatagatccgtcataaaatatccgacgaaatttgactcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 316 C;
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Pred. No. 1.4e-36;
0; Mismatches 668
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                                                                CDS
                                                                                                                              diagnosis;
                                                                                                                                            OSF-4;
                                                                                                                                                                    Sequence of murine OSF-4 cDNA
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                                                                                                                                           cadherin;
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                                                                                                                                                                                            (first entry)
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                                                              Location/Qualifiers 284..2671
                                                                                                                                           growth
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                                                                                                                                            factor;
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                                                                                                                                           osteogenesis;
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                                                                                                                                         osteoblast; therapy;
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RESULT
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line MC3T3-El and from mouse liver tissue, amplified by PCR, and
then as much common DNA as possible removed by hybridisation between
the 2 libraries. Residual El-specific DNA was amplified, inserted
into lambda gt10 and screened by plaque hybridisation. A minibank of
273 E-specific clones was recovered, their inserts amplified and
cused to screen total RNA from both cell types. One clone specific
for El was identified and sequenced. The insert from this clone was
used to screen cDNA prepd. from El RNA and the longest posn. insert
cloned in pGEM 112f (+) to give pKOT154. This insert was sequenced;
it encoded the 796 AA mouse procursor protein (Q44391/R49730). The
insert was also used to screen a cDNA bank prepd. from human
osteosarcoma to identify 2 clones encoding the 2 human precursor
proteins - QSF-4-1 and QSF-4-2 (Q44392/R49731 and Q44393/R49732
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                    New bone relat
                       03-SEP-1998;
                                                 11-MAR-1999
                                                                                                                                            arthritic disorder; asthma; immunodeficiency disease; AIDS
                                                                                                                                                        inflammatory disorder; skin disorder; tumour; atherosclerosis; restenosis; autoimmune disorder; Alzheimer's disease; peripheral neuropathy; trauma; spinal cord injury; allergy; hematopoietic disorder; skeletal disorder; neurological disord
                                                                                                                                                                                                             Human secreted protein; cancer; immune disorder; infection;
                                                                                                                                                                                                                                       DNA encoding a
                                                                                                                                                                                                                                                                  17-JUN-1999
                                                                                                                                                                                                                                                                                            X51737;
                                                                                                                                                                                                                                                                                                                     X51737 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                            WO9911293-A1
                                                                                                      Homo sapiens
                                                                                                                               transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respectively).
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DB; R49730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 79. 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related, cadherin-like OSF-4 proteins -
nosis of bone metabolic disease, and nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawai S,
                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                         human
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                                                                                                                                                                                                                                                                                                                     DNA;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                           sorder;
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12-SEP-1997;

97US-0058974

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Existance of mutations in the new polymetides are useful for preventing, the amount of the new polymetides are useful for preventing, the therapy. Pathological conditions can also be diagnosed by determining the presence of mutations in the new polymetides in a sample or by determining the presence of mutations in the new polymetides. Specific uses are described for each polymucleotide, based on which tissues they are most highly expressed in, and include developing products for the cost highly expressed in, and include developing products for the diagnosis or treatment of cancer, immune disorders, inflammatory disorders, skin disorders, tungurs, atheroscierosis, restenosis, autoimmune disorders, Alzheimer's disease, peripheral concerts, skeletal disorders, neurological disorders, arthritic disorders, asthma, immunodeficiency diseases, AIDS and transplant rejection. The polypeptides are also useful for identifying their
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
12-SEP-1997;
12-SEP-1997;
                                                   Gl protein; CASH-beta; human; caspase homologue; Fas receptor,
                                                                               Human G1
                                                                                                                                                                                                                                                        1689
                                                                                                                                                                                                                                                                                                                                                               1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 172;
Homo sapiens
                        therapy;
                                                                                                        11-JAN-1999
                                                                                                                                                              V52969
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 340 BP; 133 A; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. neurological disorders tumours, immune disorders, inflammation or haematological disorders
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les 75; Conser
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                                                                                                                                                                                                                                                                                 tcttttgatactgaaaacttttaaggtgggagggtggcaagggatgtgcttaataaatca
                                                                                                                                                             standard; cDNA; 1373
                                                                              protein isoform beta (CASH-beta) cDNA.
                                      apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                       (first entry)
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97US-0057663.
97US-0057669.
97US-0058666.
97US-0058667.
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                                                                                                                                                                                                                                                                                                                                                                                                   2.3%;
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Shi Y;
                                       cell
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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0.35;
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                                   tumour; HIV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cor with MORT binding proteins such as McA (CASP-10) and MACH (CASP-8), and thereby of binding to the intracellular domain of the FAS-R receptor, to which MORT binds, or of binding to the intracellular domain of the p55 tumour necrosis factor (TNF) receptor, to which TRADD binds and to which TRADD protein MORT-1 binds. Hence, they are considered as mediators or modulators of the signal to role in e.g. the signalling process that is initiated by the binding of FAS ligand to FAS-R, and also having a role in the signalling process that is initiated by the signalling process that is initiated by the signalling process to to regulate cell death or inflammatory processes. (II) is used to regulate cell death, and its inhibitors augment/enhance the processes. (I) and (II) regulate the FAS-R ligand or TNF effect on cells carrying an FAS-R or p55-R. Tumour, HIV-infected or other diseased cells can be treated using a viral vector encoding a viral sequence encoding (II), which kills the cell antisense oligonucleotides, introduced using the above vector, block the expression of (II) and can also regulate the above effects. These
                                                                                                                                                                    Query Match
Best Local Similarity 68.4
Conservative
                            1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This cDNA seqence codes for the beta isoform (see W78904) of novel human G1 protein. It was isolated from a human skin fibroblast cDNA library using a cDNA probe corresponding to the G1 sequence. G1-beta (also called CASH beta, CASH being caspase homologue) and a longer isoform, G1-alpha (see W78903), represent 2 splice warriests of the G1 protein whose G1 warriests of the G1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variants of the Gl protein. These Gl proteins are capable of binding to, or interacting directly or indirectly, with MORT-1 or with MORT-binding proteins such as well.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate the effects of FAS and tumour necrosis factor receptors, useful for killing of cells e.g. HIV and cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997;
03-MAR-1997;
                                                                                                                                                                                                                                                                                                                                  Sequence 1373
                                                                                                                                                                                                                                                                                                                                                                                                              effects can also be regulated using a vector encoding a ribozyme that interacts with a cellular mRNA encoding (II), and allows (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 2; 132pp; English.
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Wallach D;
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AAAAAAAAAAAAAAAAA 1703
                                                                                                                                    TGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATGTGTTAAAAA 1684
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                                                                                  RES & DEV CO LTD
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97IL-0120367.
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The present invention describes new human secreted proteins which were isolated from adult placenta, adult retina, foetal kidney, adult blood, adult brain, adult thyroid, adult bladder, adult neural continues adult testes, and adult lymph node cDNA libraries. The human content proteins, and the polynucleotides encoding them, are predicted to have biological activities which would make them suitable for the content proventing or ameliorating medical conditions in humans and continues. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating conditions. Suggested activity, activity, hammatopoiesis regulating conditions, as vaccines or suppressing activity, hammatopoiesis regulating conditions. It is not continue activity, the condition activity, hammatory activity, receptor/ligand activity, hammatory activity. Conditions in the condition activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene conditions. Active in the present human secreted proteins, and V5298 to the conditions.
           Matches
                    Query Match
Best Local
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10-AUG-1998;
11-AUG-1998;
                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                   Claim 50; Page 400; 492pp; English.
                                                                                                                                                                                                                                                                                                                                                           New polynucleotides encoding secreted human proteins, adult placenta, adult retina, fetal brain, fetal -
                                                                                                                                                                                                                                                                                                                                                                                                                                              DiBlasio-Smith
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02-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentiation;
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     Similarity 55.075; Conservative
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                                                                        1701
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, Treacy M, Ago
Smith E, Widom /
                                                                        BP;
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98US-0095880.
98US-0096068.
99US-0096068.
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98US-0087645.
98US-0093712.
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                                                                                              human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; nutritional; cytokine;
                                                                  382 A; 456 C; 494 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune stimulating; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                  2.3%;
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, Agostino MJ,
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     0;
                  Score 39;
Pred. No.
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    Mismatches
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Steininger RJ,
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in the present '--
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Bowman MR;
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                   The patent discloses a method for identifying genes that enhance levels of disease resistance if expressed in susceptible plants. The method is useful for isolating disease resistance genes (R gene) in plants. These genes confer non-host disease resistance to plants by responding to avirulence genes in plant pathogens. The R-genes identified trigger a hypersensitive response (HR) in tobacco that is dependent on the presence of the Phytophthora infestans ellcitor INF1. The genes are useful for generating pathogen-resistant transgenic plants. They can be used to e.g. Phytophthora, Exisyphe and Puccinia. The present sequence is TOB-F12 gene encoding a homologue of the 21kDa protein of Daucus carota. Expression of this gene was shown to partially control wild fire disease of tobacco.
                                                                                                                                                                                                                     expressing plants -
                                                                                                                                                                                           Claim 14; Page 90;
                                                                                                                                                                                                                         Identification of non-host plant disease resistance genes comprises expressing resistance and non-host inducible genes in susceptible
                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                          31-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOB-F12 gene; wild fire disease; tobacco; resistance gene; R gene; non-host disease resistance; plant pathogen; hypersensitive response; HR Phytophthora infestans elicitor; INF1; transgenic plant; viral pathogen;
                                                                                                                                                                                                                                                                                                                                (MONS ) MONSANTO CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogen;
                                                                                                                                                                                                                                                                                                        CMT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOB-F12 gene for controlling wild fire disease
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                                                                                                                                                                                                                                                                                                        Swords
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estans; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    "TOB-F12 protein"
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                                                                                                                                                                                                                                                                                                      Zhang
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Best Local Similarity
Matches 68; Conserv
               human c-myc promoter Pl. A full length FBP cDNA sequence was assembled from overlapping clones obtd.from CDNA libraries. Source RNAs were from undifferentiated HL60 cells, the B lymphona cell line, BJAB, and PMA/PHA stimulated pooled human peripheral blood lymphocytes (PBLS). A composite cDNA is given in Q68909 and the deduced polypeptide sequence, (67.5 kd mol. wt.) is given in R58813. Three clones from a BJAB cDNA library and three clones from an activated human PBL cDNA library contain the sequence in Q68909. Three clones from the same BJAB library and two clones from the same blab library and two clones fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding promoter P1;
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                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 57-59; 94pp; English.
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                                                                                                                                                                                                                                   DROME (DNA-binding regulator of c-myc expression) and FUSE (far upstream element) binding protein (FBP) are synonymous. A FUSE (sis required for maximal transcription of c-myc binds a factor (lor FBP). The activator cis-element is approx. 1500 bp 5' of the
                                                                                                                                                                                                                                                                                                                                                                                                             New DNA-binding regulator of c-myc of develop prods. for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-294330/36.
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The mRNA lacking these three bps would encode
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/label= A,G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c-myc; DRONE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Levens DL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                          expression and its cDNA - used therapy of disease states
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Best Local
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                   DROME (DNA-binding regulator of c-myc expression) and FUSE (far upstream element) binding protein (FBP) are synonymous. A FUSE which is required for maximal transcription of c-myc binds a factor (DROME or FBP). The activator cis-element is approx. 1500 bp 5' of the human c-myc promoter Pl. A full length FBP cDNA sequence was assembled from overlapping clones obtd.from cDNA libraries. Source RNAs were from undifferentiated HL60 cells, the B lymphoma cell line, BJAB, and pMA/PHA stimulated pooled human peripheral blood lymphocytes (PBLs). A composite cDNA is given in Q68909 and the deduced polypeptide sequence, (67.5 kd mol. wt.) is given in R58813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding
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                                                                                                                                                                                  New DNA-binding regulator of c-myc expression and its cDNA - used to develop prods. for diagnosis and therapy of disease states such as tumour formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human c-myc far upstream element (FUSE) binding protein (FBP).
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                                                                                                                                                                                                                                                                       Avigan MI, Duncan RC,
                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
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DB; R58813.
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Pred. No. 1.2;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; human; treatment; diagnosis; therapy; cancer; tumour; neurodegenerative disorder; developmental abnormality; blood disorder; fettal deficiency; blood disorder; leukemia; inmune system; inflammation; autoimmune disease; hepatic disease; renal disease; allergy; restenosis; ischaemic shock; Alzheimer's disease; cognitive disorder; schizophrenia; cardiovascular disorder; wound healing; strcke; arthritis; obesity; asthma; sepsis; acne; psoriasis; transplant rejection; infection; AIDS; metabolic disorder; ss.
This invention describes novel human genes (see 200410-200477) and the secreted proteins (see Y25711-Y25778) and fragments (see Y25779-Y25907) they encode. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 67
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                                                                                                                          Claim la; Page
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                                                                                                                                                   New isolated human genes and the secreted useful in, e.g. treatment of Alzheimer's
                                                                                                                                                                                                                                                                                        (HUMA-)
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                                                                                                                       270-271; 393pp; English.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1755
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                                                                            Cysteine protease promoter - develop plants with improved
                                                                                                                                                                                                                                                                                                                                                           Promoter; oil seed rape; cDNA clone CDCYS66; cysteine protease; disrupter protein; plant; insect pest; fungal disease; improved yield; fertility control; ss.
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                                                       Claim 23; Fig
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The present sequence encodes an oil seed rape cysteine pro the promoter for which can result the expression of a di protein gene to a suitable stage of plant development to plants with novel agronomic features, e.g. tolerance to he

herbicides disrupter provide

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modulate inflammatory function; morphological
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07-MAY-1997;
22-JAN-1998;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RS Ashikari, T., Tanaka, Y., Fujiwara, H., Nakao, M., Fukui, Y.,

Yonekura, K., Mizutani, M. and Kusumi, T.

SONE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY

PATENT: JP 1997070290-A 1 18-MAR-1997;

SUNTORY LTD

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PN JP 1997070290-A/1
PD 18-MAR-1997
PF 30-JAN-1996 JP 1996046534
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 196915 PI
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI NAKAO
MASAHIRO,

PI FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC

C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC

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/variety='japonica'
/tissue_type='petal'

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AB010708.1 GI:4185598
AB010708.1 S-aromatic acyltransferase.
Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
Gentiana triflora
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopeuphyllophytes; Spermatophyta; Magnolicphyta; eudicotyledons;
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Fujiwara, H., Tanaka, Y. and Kusumi, T. Direct Submission
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                                        CGCTACCGGTAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTC 144
                                                                     TGAACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCA---TCGGCCATCGCT 57
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                      AGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACCT
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AGCTCAACTTGTACGACTTTGATTTTGGGTGGGGGAAGCCGATAAAGTATGAGACTGTTT
                                                                                                     GGTTATCGGAATCTAATGGAATCCCTTCAAAAAGATTTCTCGGGATTACCGGATCGCCTA
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17-FBB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 196915
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
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Tanaka, Y. and Yonekura-Sakakibara, K.
Direct Submission
Direct Submission
Submitted (21-APR-1999) to the DDBJ/EMBL/GenBank databases.
Submitted (21-APR-1999) tdd., Institute for Fundamental Research;
Yoshikazu Tanaka, Suntory Ltd., Dask 18-8503, Japan
Wakayama-dai 1-1, Shimamoto, Osaka 618-8503, Japan
Wakayama-dai 1-1, Shimamoto, Osaka 618-8503, Japan
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AB026494.1 GI:7415596
acyltransferase homolog.
Gentiana triflora cDNA to mRNA.
Gentiana triflora
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnollophyta; eudicotyledons; Asteridae; euasterids
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                                                                              /gene- .........../codon_start=1
/product="acyltransferase homolog"
/protein_id="BaA93452.1"
/protein_id="BaA93452.1"
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/db_xref="g1:7415597"
/db_xref="g1:7415597"
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/db_xref="magusedikvlekcrvapppdavaeftvplsfdmmmeltsdaeh
/translation="magusedikvlekcrvapppdagulimpvdssdmmpelrykkgd
syslitarssmddbylagdhgrbsykfmullipolpepiytisgdbwlplfaldytvfsn
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fgrcivpcwvgsmhedlvuneglsvaamalgdathkrlddysgtlrgdmispprstsa
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1 (bases I to 1479)

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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Nakao,M., Fujiwara,H., Nakao,M., Fujiwara,H., Nakao,M., Nakao,M.,
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PF 30-JAN-1996 JP 1996046534
PF 17-FEB 1995 JP 95P 67159, 29-JUN-1995 JP 95P
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYU
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/tissue_type='leaves'
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anthocyanin acyltransferase.
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Sakakibara, K. Y. and Tanaka, Y.
Direct Submission
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Magnoliophyta; eudicotyledons; Asteridae;
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VFLAAEVIAAENIKKRIMDKRILETVDEKWSPEIRKALQKSYFSVAGSSKLDLYGADFGW
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                                                                                                         **C+TANS1At1On="VLETCRVGPPPDSVAEQSVPLTFFDMTWLHFPMLQLLFYEFPC
$KQHFFBSIVEKLKQSLSKTL1HFFPLSCNLIYPSSPEKMERYLSGOSVSFTIAES
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                                                                                                                                                                                    /codon_start=3
/product="anthocyanin acyltransferase"
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                                                                                                                                                                                                                                                               <1. .1343
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/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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ae; euasterids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-APR-2000
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I; Lamiales;
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Best Local Similarity 49.9%;
Matches 707; Conservative
1095 GGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCCCTTCTTGCAGATGCAAAAACT 1154
                                                                               1035
                                              969
                                                                                                                 909
                                                                                                                        975 CTTCTGACGCCCGGCTGTCCGCCTAACTACTTTGGCGACTGTCTTGCCTCATGCGTTGCA 1034
                                                                                                                                                                                  828
                                                                                                                                                                                         915 GAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGT%TTACAGCGGATTGCCGAGGA
                                                                                                                                                                                                                                                     804
                                                                                                                                                                                                                                                                     855 ATGACGTGTGGATACGTATGGACATGCATGGTCAAATCAAAAGATGACGTCGTATCAGAG
                                                                                                                                                                                                                                                                                                                     750
                                                                                                                                                                                                                                                                                                                                      795 AAGAACAAAGTACTGAATCTCAGAGGATCCGAACCGACAATACGTGTAACGACGTTCACA
                                                                                                                                                                                                                                                                                                                                                                          690 TTACCGACGGACCGCATTCGAACCACGTTCGTTTTCACCCAAATCCAAAATTAAGAAATTG 749
                                                                                                                                                                                                                                                                                                                                                                                               639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 ATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 CCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 CTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 TCGGTTTCTTTCACCATCGCAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 TCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTYGACTACCTTAAAGGTCATCAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 ATCTACCCTTCATCCCCGGAGAAAATGCCGGAGTTTCGGTA-----TCTATCCGGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 TTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGGGGAC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 AATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 CAGCTCCTTCTACGAATTCCCTTGTTCCAAGCAACATTTTTCAGAATCCATCGTTCCA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
                                  AGAATGCGGCGGCGAGAGCTGGTGGGAGAGAAAGGGGGTGTTTCTGGCAGCTGAGGTAATC 1028
                                                       AAAGCAACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATT 1094
                                                                                                   CGATTAGATCCGCCGGTTCCTGAAAATTACTTCGGGAACTGCTTATCGTACGCGCTGCCG
                                                                                                                                                                     -----GACCAAGACAACGAGGATGCATTTTTCTTGATTCCGGTCGATCTAAGGCCA
                                                                                                                                                                                                                                      GCGATTGCAGCTTATATGTGGGCTGGCATAACGAAATCATTCACAGCAGATGAA-----
                                                                                                                                                                                                                                                                                                       AAG-----GGTTGGATTCAGTCCAGAGTTCCAAGTTTAGTCCATCTCTCATCTTTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATTTTGGAACGAAATGCAAGATGTTCTTGAAATGTTCTCTAGATTTGGAAGCAAACCC 734
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTATTGGAGAAACGCGCTAAAATTTCCT-----TTGCAATCTCGTCATCCCTCA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGAATCTTCCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTATGGCCTAGAGGAA 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTATAACGGCTTGGTCTTCAATGAGCAAACACATTGAAAATGAAGATGAAGATGAAGAA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCATCAATGCTTGGGCCTATATTAACAAA---TTTGGGAAAGACGCGGGACTTGTTGTCC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTTGTAATG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCAATCGGTGCCGCTCACATTCTTCGACATGACGTG3CTGCATTTTCATCCCATGCTT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGGTTGGCACTTGAATAAGATGCAG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 171.4; DB 7; Length 1476; Pred. No. 6.1e-33; 0; Mismatches 661; Indels 49;
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AUTHORS TITLE JOURNAL REFERENCE AUTHORS		ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Db 1326 (92 92	Db 1029 Qy 1155 Db 1086 Qy 1215 Db 1146
rederspiel.N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kin,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission Stanford University, 855 California Avenue, Palo Alto, CA 94304, 4 (bases 1 to 119914) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.	yC., Lenz,C., Li,J., Liu,S. oriumi,M., Vysotskala,V.S., gis,A. and Davis,R.W. gis,A. and Davis,R.W. ,A.B., Kurtz,D.B., Conway,A r.K., Feng,J., Kim,C., Li,Y n.H., Toriumi,M., Vyotskala n.H., Toriumi,M., Vyotskala pavis,R.W. Stanford University/DNA 855 California Avenue, Palo	complete sequence. AC003027 AC003027.1 GI:4079614 HTG. thale cress. Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 119914) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenorskia T Kim, Control Buehler,E., Dunn,P., Gonzalez,A., Kremenorskia T Kim, Control Buehler,E., Dunn,P.,	99	TCTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCAGGGATTTTGAAAAAGGT 1331	

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Dec 30, 1998 this sequence version replaced gi:2734094. Bases 1-9262 of clone F21M11 overlap with bases 68998-78259 of 'TAMU' BAC clone F20D22 (ACO02411) and bases 119525-119914 of F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes with similarity to proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e-mail for correspondence: arab@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stanford
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ted (30-JAN-1999) DNA Sequencing and Technology Center,
ted (10-JAN-1999) DNA Sequencing and Technology Center,
Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEHKVAAASVELASSTSGEAKICLSFAPATGETTNLHLPSMEDLRRAMEEKCLKSYKI VHPEEFSYLGFWKDMCSCYIDLAKNSTSQLLETETVCOMSKAGDESGAWGISMPLVVVP ECEISGDGWKAISNMKDITAGEENVEIPWVNEIIEKVPSFERFYMPHSFYPQDAPVIFS LSSFSDEQSCSTSCIEDCLASEMSCNCAIGVDNGFAYTLDGLLKEEFLEARISEARDO KROVLFECEECPLERAKKVEILEPCKGHLKRGAIKECWFKCGCTKRCGNRVVQRGMHN KLQVFFTPNGKGWGLRTLEKLPKGAFICEYIGEILTIPELYQNSFEDKPTLPVILDAH WGSEERLEGDKALCLDGMFYCNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT RDIEAMEELAWDYGIDFNDNDSLMKFPDCLCGSRFCRNKKRSTKTMQTLNKA" join(13033.13488,13717.13926,14139.14514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAD10665.1"
/db_xref="G:4204284"
/db_x
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LHFGSMCCSKSKCDGMDAWIFDIDDTLLSTIPYHKKNGFFGGEKLNSTKFEDWIQKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="FZIN11.1"

/gin(7684, 7865, 7965, .8027,8122, .8160,8250, .8381

8458, .8728,8875, .9893,10003, .10256,10344, .10410,

10501, .10551,10685, .10781,10885, .10913)

/gene="FZIN11.1"

/note="Hypothetical protein"
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join(13061. .13488,13717. .13926,14139. .14316)
/gene-"F21M11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F21M11.2"
13033. .14514
                                                                                                                                                                 /protein_id="AAD10666.1"
/db_xref="GI:4204285"
                                                                                                                                                                                                                                                                                                        /note="Similar to acid
110C2T7 , gb|T42036, ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry,
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entry, AC002411."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/cultivar="Columbia"
                                                                                                                                                                                                                                                                     codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="F21M11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .119914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC002411.
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                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                   phosphatase; Location of nd 110C2XP, gb|AI100245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the databases are described as
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                                                       /gene="F21M11.6"
28007. .28465
/gene="F21M11.6"
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/protein_id="aad10668.1"
/db_xref="G1:4204287"
/db_xref="G1:4204287"
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SHTEQDSKRKROITASDAMENHLKYPKERINLAWKSADIDCNGCCSANSDDQLSSKIS
KALEQTSSNIFTICGFCQSARYSEATGEMLHYSRGRPVDGDDIFRSNVIHVBACIEM
PQVYYEGDTVKNLKAELARGMKIKCTKCSLKGAALGCFVKSCRRSYHVPCAREISRCR
WDYEDFLLLCPAHSSVUKFPNEKSGHRVSRAEFLPKINPAELCSLEQTPAFTKELVLCG
SALSKSDKKLMESLAVRFNATISRYWNPSVTHVIASTDEKGACTRTLKVLMGILNGKW
IINAAWKKASLKASQPVDEEPFEIQIDTQGCQDGPKTARLRAETNKPKLFEGLKFYFF
GDFYKGYKEDLQNLVKVAGGTILNTEDELGAESSNNVNDQRSSSIVVVNIDPPHGCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(20752. .20994,21362. .21497,21596. .21740,21825. .2:
22102. .22178,22542. .22758,22920. .23064,23343. .23442,
23599. .23693,24021. .24072,24227. .24298,24441. .24647)
/gene="F21M11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MGSSSPEARARAQVPSMILIFLEIICTVHVYTNRRKLNRDVLSA
NLNIPKRVTRRDLRFMESVISIYKSLNAAVSVHLPQLQIPNDCNYKNDALNNSNSPKH
GESEDSEMTDKDVSKRSGGTDSSSRDGSPLPTSEESDPRPKHQDWTEKQLSDHLLLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(16835. .17185,17274. .17392,17491. .1765
17795. .17885,17982. .18079,18175. .18361,18504. .18604,
18705. .19049,19134. .19349,19439. .19791,19862. .19967,
20188. .20238))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEEVTIIWQRANDAEALASQTGSRLVGHTWVLESIAGYKLHPVIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(16835. .20238)
/gene="F21M11.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDIKQESATSTPRKSPSKSPDETPIIGTVGGYWGNRSKAIDCGSASSFKGIPNTSSKYREDKSVNWHSTPFEARLEKALNNIDK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKGRTKQKQSQKENSNFIADQEEKRDSSSFGTDPQIDDITLSVKPKCRIEPKKLRNQE
LAVDASLSTWLSTSESGSECNSASMYTLTPEKLKSTSCYSKPLRINHDDRPVLCALTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDDQIIEVASNSSGSYPENHRYKNCRESDDDIEEDEFDCSDSDLDEDEEYYSDVGFSE
DSLHNPTKEVYTQDIGDKTEEIDSKLRRSNETVRDGNHYDGQGVLNPVENLTQWKSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Unknown protein; gb|AA728590 and40C3T7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(14567. .14641,14787.
16327. .16362))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(14004 . .16362)
/gene="F21M11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKEVKQYKSEKRKWLMSLGYRVWGVMGDQWSSFAGCPLPRRTFKLPNSIYYVA"
complement(join(14004. .14312,14565. .14641,14787. .15831,
15906. .16006,16327. .16362))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FESEYDAANHTPESYTEQAAKNVRDITASEQPSNAARKRICGDSFIQESSPNPKTQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD10669.1"
/db_xref="GI:4204288"
HEHGSDIIANMTKAPRVKYITFYEDSESIPGKRTAVWELDKSGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F21M11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="£21M11.4"
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ICDEAEEKCSPSTISRKRVTFDSKVKTYEHVVSEESVELSEEKNEEVESEKRSLKSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAD10667.1"
/db_xref="GI:4204286"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F21M11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .15831,15906. .16006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .21994,
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note="Unknown protein; Location of ESTs 203124T7,

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Matches
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Best Local
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  919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 CGCTACCGGTAACATTCTTCGATATCCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTCACCGTAGCAGAGTCTACTGAAACCGACTTCGACCAACTGAAGTCTGATTCCCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGCTTTCATTTGGGTAAGCTTGATCAAGACACTTGTACAAGACAGTGAAACAAAGGCCA
                                                                                                                                                                                                                                                                                                                                 GACATTTGGAGCGGTTTTGGAGCCAAAACTCTGCAAAACACAGTTCACATGTTACGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGATATCAGTGTGTTGCATGGCGTCTTGCCCAAGTTACCTCCTCCTCACGTCTCTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGATCGTTGCGGAGT---CTGACCAGGATTTTGACTACCTTAAAGGTCATCAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTCTTCTTCTCAACCAAAACTCAACTGAATCTTTCCTCCAAGACTTTGTACCCAACCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTAATCTTA 204
CATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGACTTC
                                                                                          GTGGATACGTATGGACATGCATGGTCAAATCA---AAAGATGACGTCGTATCAGAGGAAT
                                                                                                                                         GGGTTACAGAGC-----AGTCTGAGAATCAATCTCCTGTTTCTACCTTCGTGGTGACTC
                                                                                                                                                                                       AAGTACTGAATCTCAGAGGATCCGAACCGACAATACGT(TAACGACGTTCACAATGACGT
                                                                                                                                                                                                                                   TCAACAAGGTACGAGCTACATATGTCCTCTCCCTTGCT(;AAATCCAGAAGCTAAAGAACA
                                                                                                                                                                                                                                                                                                                                                                          GGAACGAAATGCAAGATGTTCTTGAAATGTTCTCTAGA?TTGGAAGCAAACCCCCTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCTCTGCCTATTCACAGCTGCAGAAACATGATCAAG()ACCCAGGCGAGGTAGGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTTCCATCTTTCGATAGATCGATAATCAAAGATCTG?ATGGCCTAGAGGAAACATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAGTATTGGATGTCATTGACCAAATCCAGCGGTAAAGATCCCGCCACGGTTCTTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAATGCTTGGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGTTGTCCGCGAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGTATAGGCAACTCAGCTACACATGTTGTAGCAGATGGAGTCACCTTCAGTCATTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTTGTAATGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCCTCGTCCCGAC-----CCTCCATATTTACACTACAACGATGGCCAAGACTCTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACTCGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACATTCCCTCTCCATCACTCTCCAACATTTCTTCCCTTACGCCGGTAAACTGATTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
612; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/gene="F21M11.7"
complement(join(29264. .31015,31312.
31782. .32033))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mntktmrlpprrvltadkrkerdafissytdnppeiakfpsppp
KLVPPPVNPISKKSSTAAAEFIGSNOLMLAGYLSHEYLTQGTLFGEQWNQARAQAESS
KIRPSHTVEPAEECEPKRKRYREVANLLRSDGAQLPGIVNPAQLARFLKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb|H76794 and 203I24xP, gb|AA605510"
/codon_start=1
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/db_xref="GI:4204289"
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Pred. No. 3.2e-18;
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Submitted (13-NOV-1997) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Str Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 4 (bases 1 to 101176)
                                                                                                                                                                                                                                                                                            Khan, S., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Kim, C., Shinn, P., Altafi, H., Bei, Q., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Theologis, A. and Ecker, J. R.
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                                                                              Direct Submission
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                                                                                                                  Submitted (25-SEP-1997) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 3 (bases 1 to 101176)
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Cheuk,R., Shinn,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bei,B., Chin,C., Chou,J., Chol, E., Conn,L., Conway,A., Gonzalez,A., Hansen,N., Chou,J., Chol, E., Conn,L., Conway,A., Gonzalez,A., Liu,A., Liu,A., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J. Direct Submission
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Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, O.,

Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,

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Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,

Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,

Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
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Direct Submission
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SGTLLVTASVCGNNINVFQIMPSRSHAARDGDLSYEWESSHVHLFKLHGGITSALVQDI
FEGOROWAY TIESUTTHETUT MEGGEN AND THE STATEMENT OF THE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CFSQQSQWVALIISSKGTCHIFVLNSSGSDAAFQPCEGEEPTRLPASSLPWWFTQSISS

NQGSLSPTAVALSVVSRIKYSSFGWLMTVSNATTAATGKYFVEVSGAVAAVFHKSVTH

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KVEPIQWWDVCRRSDWLETEERLPKSITEKQYDLETVSNHLTSHEDACLSLDMNSHFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(736. .1038,1276. .1713,1874. .2119,2205. .3032,
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                                                                                                                                                                                                                                                                                                                      INCHSKPGSIESAESSEEGSTKQMENLHDSDHMSNSIKSSLPLYPTVNGIYKEIEKNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="1"
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CDS

LSJAMNOLTGSVYHYLLRLMQLNYLDLSLNRFTGTI PARVFARPITMLOLQRNFFFGL 1QPANQYTISTVDLSY NRFSGGI SPLLSSVENLYLNSNRFTGEVPASFVERLLSANI Q TLYLQHNFLTGIQISPAAEI PVSSSLCLQYNCMVPPLQTPCPLKAGPOKKRPTTQCTE CDS

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ESTS gb|A1993651.1, db||AV538995.1, db||AV522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MRGFSSVSSWLWTSVEIGEVFLGSTTWLDAVAVAEDAVDWWVFS
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AWKCVVVLRGWGLDQIGWRSVGNWVFSVRFVAGPASSLVRDLRQDSYTSANDLVPVVV
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IGDFLQVKKIMLLLRSCFISCMIWGLILLFYCVQLITNDKFISAEHRVIANGSSEPRT
SVAIVFSTFWRAYSRVYGPIKDLLSAENPAKYRDCTLTEFSTIFSSKTLDAPKLHHFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(6700. .735
8920. .9241,9758. .10380))
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TFDAMAAHIWRSWVKALDVKPLDYNLRLTFSVNVRTRLETLKLRKGFYGNVVCLACAM
SSVESLINDSLSKTTRLVQDARLRVSEDYLRSMVDYVDVKRPKRLEFGGKLTITQWTR
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       TACTGAATCTCAGAGGATCCGAACCGACAATACGTGTAACGACGTTCACAATGACGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATATCAGTGTGTGCATGGCGTCTTGCCCAAGTTACCTCCTCCTCACGTCTCTCCGGAAG
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PQNIVCGHTLTAVFVNNSHOLILEGGSTTAVANHNSSLPEISLDGVTNSVHSFDYLTR
KWTRLNPIGDVPSPRACHAAALYGTLILIQGGIGFSGGDVXHLDWTNNKWIKFLV
GGETPSPRYGHWDIAACHAYALVIFSGNNGNEILDDTWALDTROPESWDRLNPSGNQPS
GRMYAAGSSREDGIFLLCGGIDHSGVTLGDTYGLKMDSDNVWTPVPAVAPSPRYQHTA
VFGGSKLHVIGGILNRARLIDGEAVVADTNQPETSASGANRQNQYQLMRRCHHAAAASF
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/db_xref="GI:9280670"
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                                                                          Nakamura,Y.

Direct Submission

Submitted (13-OCT-1999) to the DDBJ/EMBL/GenBank databases.

Yasukazu Nakamura, Kazusa DNA Research Institute, Labbratory of Gene Structure 2; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamufekazusa.or.jp, URL:http://www.kazusa.or.jp/gene-s2/,

Tel:81-438-52-3935, Fax:81-438-52-3934)

Location/Qualifiers
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopreuphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
'----- nocidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                Structural Analysis of Unpublished (1998) (bases 1 to 82360)
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/organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="3"
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                        AGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACGA 1126
                                                  TTGTCGGGTCGGGAGATTTCGACGTGAAAGCAGAACCAATATTGGAAGAAGGAGGAA
                                                                                                       CATCAGACTTTCGGTCACGGTTAAACCCTCCGTTACCGCCGACGTTCTTCGGGAACTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted (20-JUL-2000) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, odtown@tigr.org * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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Arabidopsis thaliana chromosome ? clone
IN PROCRESS ***, 8 unordered pieces.
AC074226. GI:9295757
HTG: HTGS_PHASE1.
thale cress.
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Town,C.D. and Kaul,S.
Direct Submission
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Magnolophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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10514: contig of 10514 bp in length
10564: gap of unknown length
31604: contig of 21040 bp in length
31630: contig of 5976 bp in length
37630: contig of 5976 bp in length
37680: gap of unknown length
44842: contig of 7162 bp in length
44892: gap of unknown length
69074: contig of 24182 bp in length
69124: gap of unknown length
135012: contig of 65888 bp in length
135062: gap of unknown length
159445: contig of 64383 bp in length
159445: contig of 24383 bp in length
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                                        CATCAGACTTTCGGTCACGGTTAAACCCTCCGTTACCGCCGACGTTCTTCGGGAACTGCA 111244
                                                           CAGCGGATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTATCTTTGGCAACTGTC
                                                                                                                                                                                                                   AAGACATCAAGAAGCTA----CGTGAACGAGTGGAGACCGAGTCACACGCTAAGCAGCTCC
                                                                                                                                                                                                                                                                           TGTTTCCTTCCAAAATAATTGGATCCGATATTCTCCGAGTCACGTACCGGTTAACTCGAG
                                                                                                                            ATGACGTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTA 957
                                                                                                                                                                         CTGAAATCCAGAAGCTAAAGAACAAAGTACTGAATCTCAGAGGATCCGAACCGACAATAC
                                                                                                                                                         -----GCAPACCCCCTCGATTCAACAAGGTACGAGUTACATATGTCCTCTCCCTTG
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                                                                                                                                                                                                                                                                                                                                                                                            CTCTGCCACACGATCTAGTACCGTCTTTAGATCGTATCATTGTTCAAGACCCCAACGGGAC 111577
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-----CGTCATGCGTTGCAAAAGCAACACATAAAGAGTTAGTTGGGGATAA
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/db_xxef="taxon:3702"
/chromosome="?"
/clone="IGF-F27B9"
28890 c 29784 g 52486 t 3
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Pred. No. 1.
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                                                                                                                                                                                                                             Submitted (18-AUG-1998) to the DDBJ/EMBL/GenBank databases, Yasukazu Nakamura, Kazusa DNA Research Institute, Laborator Gene Structure 2, 1532-3, Yana, Kisarazu, Chiba 292, Japan (B-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3935)
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* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Ronning,C.M.,
KOO,H., Fujli,C.Y., Utterback,T., Barnstead,M.E., Bowman,C.L.,
White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana 'IGF' BAC 'F7F7' genomic sequence near marke
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TATGTGATTCAGTCCAGGGATTTTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAAG
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                                                               TTTGGATGGGGAAAGCCTGCAAAATTTGACATTACCTCTGTTGATTATGCAGAATTGATT 1298
                                                                                                CAGGTACACAGA-TTGGATCCATTGCCGGTTCGAACCAGTTTGGGCTATACGGGTCAGAT
                                                                                                                               CCTTCAAAAAGATTTCTCGGGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGAT 1238
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/db_xref="taxon:3702"
/chromosome="I"
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Best Local Similarity 56.7%;
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GTCTTTTTCAACAATGGTTT 16487
                             AAAAATCTTTGAAGAAGGCTT 1399
                                                       TAAAGTTGATATTGTCTCCATTGACCAAGGAGAAGCGATCGCAATGGCTGAGAGACGTGA 16406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (09-JUN-1999) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laborator
Gene Structure 2: 1532-3, Yana, Kisarazu, Chiba 292, Japan
(E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural Analysis of Unpublished (1999) 2 (bases 1 to 85690)
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15199 c 15751 g 26784 t
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/strain-"Columbia"
/db_xref-"taxon:3702"
/chromosome-"3"
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                                                                                                                                                                                                                                                          Score 61.8; DB 7;
Pred. No. 5.6e-05;
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  GTCTTTTTTCAACAATGGTTT
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                                         AAAAATCTTTGAAGAAGGCTT 1399
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* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1 (bases 1 to 136047)

11(n,X., Kaul.S., Town,C.D., Benito,M., Creasy,T.H., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.

Arabidopsis thaliana 'IGF' BAC 'F7F7' genomic sequence near marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 136047)
Town, C.D. and Kaul, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="I"
/clone="IGF-F7F7"
/ 22872 c 22213 g 44783 t 1
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                                                                                                                                                                                                                                                                                                                                                                     3.6%;
56.7%;
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Pred. No. 5.8e-05;
0; Mismatches 87;
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*** SEQUENCING
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Job time: 6483 sec

us-08-894-356c-1.rst

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em_esthum7:*
em_esthum10:*
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em_gss12:*
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qb_gss13:*
qb_gss13:*
qb_gss14:*
qb_gss16:*
qb_gss16:*
October 20, 2000, 01:35:37 ; Search time 1792.79 Seconds (without alignments) 5873.147 Million cell updates/sec
                                                                                                                                            14379728
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                  7189864 seqs, 3091403243 residues
                                                     OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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9b_9ss18:*
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9b_9ss20:*
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em_9ss16:*
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 1117:
1118:
1120:
1221:
122:
123:
124:
126:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		4257 EST4053	61049 EST29688	36185 EST40726	30934 EST35677	50 EST29751	145	3336	37239	90650	280	5584		AUK16206 EST330160	200	40958	3276	1227	583		571	96 A	555	D ESTZBUL	7 2	2527 NF056D0	1948 EST3340	3747 EST3550	3420	0186 AV54018	AV523212	20000	8087 AU038087	5291	5972 EST31859	480 T24H11-T	323 zw21b07.	044 sf30a0	34071 Ara	45 C92395	52875 Dro	122 HTM1
SUMMARIES	ΩI		BE434257	1611	361	3093	105	9044	3333	3723	5065	5028	AL386584	0000	1620	3393	1095	3027	\sim	3658	~	3157		BE323055	7.5	AW587016	2	7494	5374	342	BIOI	AV523212	1000	AU038087	952	3697	B09480		AW310044	1 CNSOOWUX	C92395	CNSUCZMU	BE440122
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ALIGNMENTS

REFERENCE I; Solanaless, Solanaceae; Solanum, Lycopersicon. AUTHORS Alcala.J. Verballov.J. White, N. van der Hoeven, R. S., Holt II. E., Liang, P. V. Preballov.J. White, N. van der Hoeven, R. S., Holt II. E., Liang, P. Hansen, T. S., Creven, M. B., Bowman, C. L., Rouning, C. M., Wartin, G. B., Glovannoni, J. J. and Tanksley, S. D. Nierman, W., Fraser, C. M., Martin, G. B., Glovannoni, J. J. and Tanksley, S. D. Internation of ESTS from tomato fruit tissue, breaker stage commerce in the contact: David Frisa. Contact: David Frisa. Internation of ESTS from tomato fruit tissue, breaker stage commerce in the contact: David Frisa. Internation of ESTS from tomato fruit tissue, breaker stage commerce in the contact: David Frisa. Internation of ESTS from tomato fruit tissue, breaker stage commerce in the first of the sequence. Authorise from the fruit of the contact of the fruit of the sequence. Authorise from the fruit of the fruit of the breaker stage contact of the fruit of the seads and the sequence. Authorise fruit were harvested at the breaker stage of the fruit of the seads and the fruit of the seads and the seads and the fruit of the fruit of the seads and the seads and the fruit of the seads and the fruit of the seads and the fruit of the seads and the seads and the fruit of the fruit of the fruit of the seads and the fruit of the seads and the fruit of the seads and the fruit of the fruit of the fruit of the fruit of the seads and the fruit of the fruit of the fruit of the seads and the seads

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Solamates; Solamaces; Solamaces; Solamaces; Solamaces; Solamaces; Solamani, Lycopersicon.

1 (bases I to 606)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Opton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of Esrs from tomato fruit tissue
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                                                                                                                                                                                                                                                                                                              AW221049 606 bp mRNA EST 07-DEC-1999
EST297518 tomato fruit mature green, TAMU Lycopersicon esculentum
cDNA clone cLEF3F1, mRNA sequence.
AW221049
AW221049.1 GI:6532733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-vector: pBlueScript SK(-); Site 1: EcoR1; Site_2: Xhol; cLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                    612 TCCGCGAATCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTATGGCCTAGAG 671
                                                               GTAATGTTCATCAATGCTTGGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGTTG 611
                                                                                 79 AGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGT 138
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/clone="cLEF3F1"
/clone_lb="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
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/lab_host="SOLR"
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    606
    /organism="Lycopersicon esculentum"
/cultivar="TA496"

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Contact: David Frisch
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Lycopersicon hirsutum.
Lycopersicon hirsutum.
Lycopersicon hirsutum
Eukaryota; Viridipjantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridipjantae; Solamas, core eudicots; Asteridae; euasterida
1; Solamales; Solamaceae; Solamum; Lycopersicon.
1 (bases I to 603;
Ven der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Generation of ESTs from wild tomato (Lycopersicon hirsutum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW616119 603 bp mRNA EST 24-MAR-2000 EST2596884 L. hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHT6C7 3', mRNA sequence.
AW616119 GI:7323152
318
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/db_xref-"taxon:62890"
/clone-"cLHT6C7"
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Clemson University Genomics Institute
Clemson University
100 University
Tel: 864 656 4366
Fax: 864 656 4293
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Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
5 prlme sequence.
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Best Local Similarity
Matches 262; Conserv
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I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                       3;
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Jaclas, J. Vrebblov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
/tissue_trpe="trichome"
/dev_stage="mixed stages"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded
mixture of cells which is highly enriched for trichome
likely with minor contaminations of other types of leaf
cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE436185 542 bp mRNA EST 24-JUL-2000 EST407263 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG31A19, mRNA sequence.
BE436185 GI:9434028
                                                                                                                                                                                                                                                                                                                  1023 TCATGCGTTGCAAAAGCAACA---CATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTT 1079
                                                                                                                                                                                                                                                                                                                                                                             GCAGTTGCAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTT 1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1200 ATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCA 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1260 AAATTTGACATTACCTC-----TGTTGATTATGCAGAATTGATTTATGTGATTCAG 1310
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                                                                                                                                                                                                                                                    963 GATTGCCGAGGACTTCTGACGCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCG 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 GCGGTAGAATCAATTGGAGAAGTCATTCAAGAAAAATGAAGGATGATGAATGGGTCCTT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 AATGGTG-----ATTGGTTAAAAGTATTAGACAACATAGATGTGATTCGATCATTTTCA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                        Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                       18;
                                                                                                                                                                                         DB 23; Length 603;
                                                                                                                                                                                                                      Indels
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Pred. No. 4.8e-18;
0; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                                                                                         6.3%;
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                                                                                                                                                                                         Query Match 6.3
Best Local Similarity 57.2
Matches 263; Conservative
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Lycopersicon esculentum
Eukaryota, Viridiplantee, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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EST356777 tomato fruit mature green, TAMU Lycopersicon esculentum
CDNA clone cLEF42M23 5', mRNA sequence.
AW930934 GI:8106335
                                                                                                                                                                                                                                                /note="Vector: paluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1190 ATTICICGGGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGG 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1013 CTGTCTTGCGTCGTTGCGTTGCAAAGCAACA---CATAAAGAGTTAGTTGGGGATAAAGG
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                                                                                         /db_xref="taxon:4081"
/clone="cLEG31A19"
/clone=llb="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="Preaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1250 AAAGCCTGCAAAATTTGACATTACCTCTGTTGATTATGCAGA 1291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.3%; Score 107.2; DB 35;
llarity 56.7%; Pred. No. 5.9e-18;
Conservative 0; Mismatches 188;

    .542
    /organism="Lycopersicon/cultivar="TA496"

Location/Qualifiers
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LOCUS
DEFINITION
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                      Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Farser, C.M., Martin, G.B., Tanksley, S.D. and Glovannoni, J. Generation of Ergr from tomato fruit tissue (1999)
Contact: David Frisch
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 436
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /close_lb-remato fruit mature green, TAMU"
//tissue_lype="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="80LR"
/l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seeds and locules were discarded prior to freezing the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GATACAAACGGATATCCTGAGTTACGTTA----TGTGACAGGAGATTCTGTGTCTGTT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 ATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAACTGGTAGATTCC 389
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Pred. No. 1.8e-16;
0; Mismatches 209; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lycopersicon
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEF42M23"
                                                                                                                                                                                                                                                                                                                                                                                                         prime sequence.
Location/Qualifiers
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Best Local Similarity 54.0%;
Matches 256; Conservative
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      (bases 1 to 497)
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RESULT AW221050

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/organism="Lycopersicon esculentum"
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/clone="lomato fruit mature green, TAMU"
/clone="taxon:4081"
/clone="taxon:4
                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum
Enkaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermaiophyta;
Bagnollophyta; eudicotyledons; core eudicots; Asteridae; euasteridae;
Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 583)
Alcala,J., Wrebalov,J., White,R., Matern,A.L., Holt,I.E., Llang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Mattin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of EST; from tomato fruit tissue
Uppublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä;
         ST 07-DEC-1999
Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 CTGTGTCTGTTACTTTTTCGAGACTGATATGAATTTCAATTATCTCATTGGTGACCATC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 AGTTATCGCTACCGGTAACACTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 CCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 CTCTTAAAAATTCACTCTCCCTCACTCTCAAACACTATACGCCCTTAGCCGGAAACGTTG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 CGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAAC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 TGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 583;
EST297519 tomato fruit mature green, TAMU CDNA clone cLEF3F3, mRNA sequence.
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illarity 52.4%; Pred. No. 2.7e-16;
Conservative 0; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Exa: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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1. .583
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Best Local Similarity
Matches 299; Conserv
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                                                                                                                                                                                                                                                                                                tomato.
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161

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821

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RESULT

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Glycine max
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bagnollophyta; eudicotyledons; core eudicots; Rosidae; eurosida I;
Enbales; Fabaceae; Papilionoideae; Glycine.

1 (bases 1 to 687)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
Shoemaker, R., Kaim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
'A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
'R., Ferson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
'R., Waterston, R. and Wilson, R.
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW102336 687 bp mRNA EST 06-DEC-1999 sd86d06.yl Gm-c1009 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1009-1284 5' similar to TR:Q92WB4 Q92WB4 F21M11.13 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40RP from Gibco
High quality sequence stop: 431.
                                                                              822 TCCG------AACCGACAATACGTGTAACGACGTTCACAATGACGTGTGGATAC 869
                                                                                                                                                                                                                                                                                                                                                                         306 CGGGGTAGTAGTACTACTCTAACTCATGTAACATCTTTTACTGTAACGAGTGCTTAT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACAAATTCGGTGGACATGAACAATTCTTATCGAATGAGCTAATTCCATTTTATGATAGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Far: 314 286 1810
Fax: 314 286 1810
                                                  642 TCGATAATCAAAGATCTGTATGGCCTAGAGGAAACATTTTGGAACGAAATGCAAGATGTT
                                                                                                                                                                                TATGTCCTCTCCCTTGCTGAAATCCAGAAGCTAAAGAACAAAGTACTGAATCTCAGAGGA
                                                                                                                                                702 CTTGAAATGTTCTCTAGATTTGGAAGCAAACCCCCTCGATTCAACAAGGTACGAGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                        870 GTATGGACATGCATGGTCAAATCAAAAGATGACGTCGTATCAGAGGAATCATCGAACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 GAAAATGAGCTCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGACTTCTGACGCCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      990 TGTCCGCCTAACTACTTTGGCAACTGTCTTGCGTCATGCGTTGCAAAAGCAACA 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AW102336
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AW102336
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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Y., Bowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBlueScript SK(-); Site_1: EcoR1: Site_2:
Not): cLED - Tomato Carpel EST Library. OilgodF-primed and
directionally cloned CDNA in vector Lamda ZAP II with 5'
and 3' ends located at the EcoR1 and XhoI sites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum subrayophyta; Tracheophyta; Spermatophyta; Magnollophyta; Sudicotyledons; core eudicots; Asteridae; euasterids i; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 549)
Alcala, J. Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Llang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Frascr, C.M., Venter, J.C., Martin, G.B., Tanksley S.D. and Glovannoni, J.
Generation of EsTs from tomato carpel tissue
Unpublished (1999)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI490445 549 bp mRNA EST 29-JUN-1999 EST248771 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED21J4, mRNA sequence.
379 TGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACCA 438
                         CACCGGGGGTCCAACTAGCCCGCTCTTAGCCATTCAGGTGACACTTTTTCCGAATCTTG 469
                                                                                                                                                                                                                         582 AACAAATTTGGGAAAGACGCGGACTTGTTGTCCGCGAATCTTCTTCCATTGTTCGATAGA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9. CATCATGTTGTTGGTGTGATGGAGCTATAGGCAGGGTTCATTAAGGCGTGGGCTCTACTC 68
                                                                                                                                                                                             GCATAGCCGTGGCTCTGACGCCACATCATTCCAGTTGCAGATGCTAAAAGTTTTGTAATGT
                                                                                             439 TGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 97.4; DB 11; Length 549; 53.2%; Pred. No. 2.4e-15; ive 0; Mismatches 232; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 549
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
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/clone_lib-"tomato ovary, TAMU"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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Tel: 864 656 4366
Fax: 864 656 4293
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56.8%; Pred. No. 7.8e-14;
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                             //note="Vector: possession of the property of the property of the mana was isolated from entire roots of 2-month-old "Williams" plants that were greenhouse grown in 5-gallon pote: To suppress nodulation, Black Gold all-Purpose potting soil was supplemented with: 0.36g/L available phosphoric acid (P205), 20mg/L urea N. 0.16g/L S, 0.49mg/L B, 2.5mg/L Cu, 0.15g/L Fe, 13.5mg/L Wn, 0.26mg/L Mo, 14mg/L Zn, 20mg/L Ca, and the following nutrients in a slow-release form (osmocote): 0.16g/L ammonia N, 0.185g/L nitrate N, 0.35g/L available phosphoric acid, and 0.35g/L soluble potash. No nodules were visible on the roots at harvest. Stratagene's cDNA Synthesis Rit (catalog #200401) was used to synthesize the CDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated.

Stratagene's first-strand synthesis was used (GAGAGAGAGAGACACACACCACCAG(T)-18]. After second-strand synthesis is, the CDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the CDNA constructs were strategioned at the CDNA constructs were stated into Stratagene's pluescript II XH end per digested with EcoRI and XhoI, and phosphorylated). Both the white and ligated into Stratagene's pluescript II XH++) that had been digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with CDNA inserts. This library as constructed by Dr. Paul Kelm and Dr. VIrginia Coryell." 5 others
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               /lab_host="XL10-Gold"
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/tissue_type="flower"
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van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
, F., Hansen, T.S., Caven, M.B., Bowman, C.L., Ronding, C.M., Nierman
, W., Fraser, C.M., Martin, G.B., Glowanno, J.J., and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, anthesis
Unpublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Fex: 864 656 4366
Fex: 864 656 4293
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529 ACCATATGTCTCACCTTCAACCACCTTGCCAGCGACGCCAAGTCACTTCACCATTTCATC
                                                                                                                                                     AATGCTTGGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGTTGTCCGCGAATCTT
                                                                                                                                                                                                                                                                                            589 AAGTTCTGGGCCTCTCTTTGCANAGCANAAGGAAACATGGCTTNNCTTTCAACCTCTNTG
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1100 AGCCATTGAAAAGAGGTTGCACAACGAAAAGGCGTTCTTGCAGATGCAAAAACTTGGTT 1159
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//organism="Lycopersicon esculentum"
//oullivar="TA496"
//oullivar="TA496"
//olone="Cisil13N5"
//clone="Lib="tomato germinating seedlings, TAMU"
//tissue_Lype="Whole seedlings"
//tissue_Lype="Whole seedlings"
//dow_stage="7" days post imbibition
//note="Vector: pBlueScript $K(-); Site_1: EcoRl; Site_2:
Xho1; 7 days post imbibition on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
to two centimeters in seeds not showing obvious signs of
germination were discarded."
86 a 114 c 75 g 168 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S, Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronnning,C.M.,
Nierman,W., Fraser,C.M., Glovannoni,J.J., Martin,G.B. and Tanksley
                                                                                                            1280 TGATTATGCAGA-----ATTGATTTATGTGATTCAGTCCAGGGATTTTGAAAAGG 1330
                                                                                                                                                                                       1331 TGTGGAGATTGGAGTATCATTGCCTAAGATTCATATGGATGCATTTGCAAAAATCTTTGA 1390
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                                                                                                                                126 AAAAGTATACGACAATGTAGATGTGATTCGATCATTTTCAATTGCTGGATCGCAAAAACA 185
                                                     186 TGACTTATATGCTGCTGATTTTGGATGGGGAAGAGCCGCAAAGTTGGAATTCATTTCCAT 245
                                                                                                                                                                                                            526 AAGGCATGTTGGAAGGGAAGGGTTTAAAATTGCGGTAGAATCAATTGGAGA 467
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                                   1220 CGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                 EST329104 tomato germinating seedlings, TAMU Lycopersicon esculentum cDNA clone cLE113N5 5', mRNA sequence.
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Pred. No. 8.4e-14;
0; Mismatches 149;
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Tel: 864 656 4366
Ex: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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Clemson University
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AW650650.1 GI:7411888
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Contact: David Frisch
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Lycopersicon esculentum
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Asteridae; euasterids
1; Solanales; Solanacaes; Solanum; Lycopersicon.
1 (bases 1 to 518)
Alcalaju, Verbalov, J. White, R., van der Hoeven, R.S, Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronnning, C.M.,
Nierman, W., Fraser, C.M., Glovannoni, J.J., Martin, G.B. and Tanksley
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/tissue_type="whole seedlings"
/tissue_type="whole seedlings"
/dev_stage="7 days post imblition"
/note="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="typ
                                                                                                              1160 ATCGGAATCTAATGGAATCCCTTCAAAAGATTTCTCGGGATTACCGGATCGCCTAAGTT 1219
                                                                                                                                                                                                                                                                                                                                       1220 CGATICGTATGGTGTAGATITIGGATGGGGAAAGCCTGCAAAAITIGACATIACCTCTGT 1279
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                                                                                                                                                                               AW650280 518 bp mRNA EST 04-APR-2000 EST328734 tomato germinating seedlings, TAMU Lycopersicon esculentum cDNA clone cLEI12F13 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                             466 AGTCATTCAAGAAAAATGAAGGATGATGAATGGGTCCTTAATGGTGA-----TTGGTT
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Location/Qualifiers
1. 518
/organism="Lycopersicon esculentum"
/oultivar="TR496"
/db_xref="taxon:4081"
/clone="cLE112F13"
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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AW650280.1 GI:7411518
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Contact: David Frisch
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Anote—Vector: pBluescript pSK: Site_l: EcoRI; Site_2:
Xhoi; M. truncatula sterilised seeds were germinated for
72h at 25 C. before transplanting into a 1/3 Epoisses soil
27/3 calcined Terragreen mix in the presence of onion
root fragments colonized by the arbuscular mycorrhizal
fungus Glomus intraradices (Schenck & Smith, isolate LPAB). The plants were watered every day and twice a week with
a modified nutrient Long Ashton solution without phosphate
but with a high level of nitrate. After 3 weeks RNA was
extracted from whole root systems. CDNA was prepared from
polyA+ enriched RNA. The CDNA was directionally ligated
into Uni-zap XR vector from Stratagene and packaged using
Glapack Gold packaging extracts. Plasmids containing cDNA
inserts were mass-excised from phage stocks using Exassit
helper phage and propagated in SOLR cells. Clone ordering
sequencing was performed by the Centre National de
finnaal origin."
                                          /tissue_type="arbuscular mycorrhiza"
/dev_staye="harvested 3 weeks post inoculation with Glomus
intraradices"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       958 CAGCGGATTGCCGAGGACTTCTGACGCCCCGGTGTCCGCCTAACTACTTTGGCAACTGTC 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1078 TTGCAGTTGCAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTC 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCAGAT-----GCAAAAACTTGGTTATCGGAATCTAATGGAATCCCTTCAAAAGAT 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICTCGGGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAA 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1312 CCAGGGATTTTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAAGATTCATATGGATG 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 crerrearreraegreaegeriegarecaecaarraargaaarrarrigegaarrera 60
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EST305729 KV2 Medicago truncatula cDNA clone KV2-1104, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 526;
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llarity 50.6%; Pred. No. 3.7e-12;
Conservative 0; Mismatches 221;
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Best Local Similarity
Matches 234; Conserv
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Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bagnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.

1 (bases 1 to 526)
Journet, E. P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL386584 526 bp mRNA EST 03-AUG-2000
MtBC35E10R1 MtBC Medicago truncatula cDNA clone MtBC35E10 T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula ESTS from endomycorrhizal roots
Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
                                        114 TGGTTGCACTTGAATAAGATGCAGTCCCTTCTGTTTTACGACTTTCCGTACCCAAGAACA 173
                                                                                                                                        233
                                                                                                                                                   413
                                                                                                                                                                                                           TACGTTCCGCTTAGCGGAAATTTGTTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTT 293
                                                                                                                                                                                                                                                 124 TATACGCCCTTAGCCGGAAACGTTGCTTGTCCACTAGATACAAACGGATATCCTGAGTTA 183
                                                                                                                                                                                                                                                                                          294 CAGTACTCCCGTGATGAGGGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGAT 353
                                                                                                                                                                                                                                                                                                                                                    237
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               Gaps
                                                                CATTICITGGACACIGITATCCCTAATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACAC
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                                                                                                                                                                                                                                                                                                                                  184 CITTATGTGACAGAGATGCTGAGTCTGTTACTTTTTC-----GAGACTGATATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 GGACATGAACAATTCTTATCGAATGAGCTAATTCCATTTATGA 518
    Mismatches 247;
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/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBC35E10"
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  Conservative
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Matches 268;
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Best Local S
Matches 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marinost ... coli strain SOLR"
//dab.host="Re. coli strain SOLR"
//note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
Xnoi; cDNA was prepared from poly4+ enriched RNA. The
CDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in SOLR cells."
a 172 c 76 g 217 t
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                        (bases 1 to 705)
VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                         ESTS from roots of Medicago truncatula after Rhizobium inoculation Unpublished (1999)
Contact: Vandenbosch K
Department of Biology
Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                        More information is availble at. . (and for clone ordering info) http://chrysie.tamu.edu/modloago Seq primer: Skmod (CTA QAA CTA gtg gAT CC). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="KV2"
/tissue_type="Seedling roots"
/dev_stage="2 days post-inoculation with Sinorhizobium
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               946 ACTTCAGTTTTACAGCGGATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTACT 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAAAAAGATTTCTCGGGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTG 1242
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                     Magnoliophyta; eudicotyledons; core eudicots
Fabales; Fabaceae; Papilionoideae; Medicago.
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Pred. No. 4.5e-12;
0; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                              College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                          Email: kate@mail.bio.tamu.edu
Texas A&M EST name:T250085e
TIGR seguence name:MTAAZ86TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="KV2-1104"
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Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Eabales; Fabaceae; Papilionoideae; Medicago.

1 (bases 1 to 788)
VandenBosch, K., Hur, J., Beremand, P., Peng, H. and Ellis, L.
ESTS from uninoculated seedling roots of Medicago truncatula
Unpublished (1999)
Contact: VandenBosch K
Department of Biology
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Xhoi; cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Giapack III Gold
packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in SOLR cells."

188 c 100 g 262 t lothers
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286 TTGTTGAGAGTAGAGATTTTGAGGGTGGAATTGAGATAGGGTTAGCTTTGCCTAAGAGTA 227
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                                                                                                                                                                                                                                                                                 BE187619 788 bp mRNA EST 22-JUN-200
EST336180 KV0 Medicago truncatula cDNA clone pKV0-1613, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium melliloti (0 hour)"
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llarity 51.5%; Pred. No. 6.7e-12;
Conservative 0; Mismatches 224; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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/clone_lib="kV0"
                                                             1363 ATATGGATGCATTTGCAAAATCTTTGAAGAAGG 1396
                                                                                                     226 AAATGGATATTTTCACCTTTTTCTTCAAGAATGG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 2707
Fax: 409 845 2891
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Texas A&M University name:T260795e
TiGR sequence name:MTGAU50TK
More information is available at.
                                                                                                                                                                                                                                                                                                                                                                                                             GI:8666803
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BE187619.1
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Lycopersicon hirsutum.
Lycopersicon hirsutum
Lycopersicon hirsutum
Eukaryota; Viridiplantee; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantee; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; Solanaceae; Solanum; Lycopersicon.

1. Solanales; Solanaceae; Solanum; Lycopersicon.

1. (bases 1 to 487)

yan der Howenn, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang der Howenn, R.S., Bowman, C.L., Ronning, C.M., Nierman, W., Fr., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Generation of ESTs from wild tomato (Lycopersicon hirsutum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="L. hirsutum trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells which is highly enriched for trichome
likely with minor contaminations of other types of leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                     AW616206 487 bp mRNA EST 24-MAR-2000 EST307245 L. hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHT1D15 5', mRNA sequence.
                                                                                                                                                                             349
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                                                                                              410 TCCATTGGCCTAGCTTTCATCATGTTGCTGATGGAAGAACCTTCCACAATTTCATC 469
             CCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACTCGATA 323
                                          --CGTTCCCTCGCTTGATCTAACCGAACCTCGAATTTACTCTTAACAACTCGGTT 235
                                                                                                                                            GATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACCATGCAA 443
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                                                                                                                                                                                                                                                                         GCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTTGTAATGTTCATC 563
                                                                                                                                                               ACTITGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAAGGTCATCAACTGGTA
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/db_xref="taxon:62890"
/clone="cLHT1D15"
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Pred. No. 1.8e-11;
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Clemson University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: David Frisch
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Fax: 864 656 4293
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COMMENT
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DB 23; Length 487;

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                                                                                                                                                                                                        TTCTTGGACACTGTTATCCCTAATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTAC 236
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                                                         CCATCTGACACAACAGATGTCGAGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGG 116
   Gaps
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Mismatches 227; Indels
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Search completed: October 20, 2000, 02:07:23 Job time: 1906 apr

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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77.8	77.8	87.8	102.2	106.4	153.8	153.8	172.6	193	193	763.6	765.4	Score		
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JP 1997070290-A/4.
                       C12R1:865),
PC (C12N9
CC strand
CC topolc
FH Key
FH Source
FT source
                                                                                                                                               Patent: JP 1997070290-A 4 18-MAR-1997;

SUNTORY LTD
OS Perilla ocimoides
PN JP 1997070290-A/4
PD 18-MAR-1997
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI,
MASAHIRO.
                                                                                                                                                                                                                                                1 (bases 1 to 1479)
Ashikari, T., Tanaka, Y., Fujiwara, H., Nakao, M., Fukui, Y.,
Yonekura, K., Mizutani, M. and Kusumi, T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070290-A 4 18-MAR-1997;
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                                                                                                                         PI FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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                                                                                     strandedness:
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33 AC069470
34 AC032048_0
1 CNSOTEQ
7 DDGC0170
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7 DDGC07647
7 DDGCNPA
1 PFMAL13P2_3
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AC074226 Arabidops
AL035477 Plasmodiu
AE001425 Plasmodiu
AC069470 Arabidops
X77854 P falciparu
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AE001397 Plasmodiu
U87514 Dictyosteli
AC010989 Homo sapi
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AC023048 Mus muscu
AL359239 Homo sapi
U60170 Dictyosteli
AJ005398 Dictyoste
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AC004688 Plasmodiu
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AATCATTCACAGCAGATGAAGAC --- CAAGACAACGAGGATGCATTTTTCTTGATTCCGG
                       GTTTAGTCCATCTCTCATCTTTTGTAGCGATTGCAGCTTATATGTGGGCTGGCATAACGA
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/organism="unidentified"
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                                     2 (bases 1 to 1476)
2 (bases 1 to 1476)
Sakakibara,K.Y. and Tanaka,Y.
Direct Submission
Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Reiko Sakakibara, Suntory Research Center, Fundamental Research, Plant Biotech; Shinamoto-cho, Wakayamadai, 1-1-1, Mishima-gun, Osaka 618-8503, Japan (E-mail:Keiko_Sakakibara@suntory.co.jp, Tel:+81-75-962-8807, Fax:+81-75-962-8262)
Location/Qualifiers
                                                                                                                                                                  Sakakibara, K.Y., Tanaka, Y., Mizutani, M.F., Fujiwara, H. Ashikari, T., Yamaguchi, M. and Kusumi, T. Molecular and blochemical characterization of a novel hydroxycinnamoyl CoA: anthocyanin 3-C-glucoside-6
                                                                                                                                                                                                                              Perilla frutescens
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnollophyta; eudicotyledons; Asteridae; euasterids
Lamiaceae; Perilla.
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Perilla :
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                                                                                                                               TCGACCGATCGCTCGTGAATTATCCGCCTAAATTGGACACATATTTATGGAACAACGCGC
                                                                                                                                                                  TGAGCAAACACATTGAAAATGAAGA---TGAAGATGAAGAATTTAAATCTTTGCCAGTTT
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/product="anthocyanin acyltransferase"
/prodein_id="BaA93475.1"
/db_xref="gi:7415646"
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/translation="VIETCRVGPPPDSVAEQSVPLTFFDMTWLHFHPMLOLLFYEFPC
SKOHFSESIVPKLKQSLSKTLTHEFPLSCNLIYPSSPEKMPEFRYLSGDSVSFTIAES
SDDFDDLVGNRPESPVRLVNFVPKLPPIVEESDRKLVGVAQQVTLFPGRGVGIGIAT
HHTVSDAPSFLAFITAWSSMSKHIENDEDEEFKSLPVPDRSVIKYPTKPDSIVBRNA
LKEPLOSRHPSLPTDRIRTTFVFTQSKIKKLKGWIQSRVPSLVHLSSFVAIAAYMWAG
ITKSFTADEDQDNEDAFFLIPVDLRPRLDPVPENYFGKJALFRMRRRELVGEKG
VFLAAEVIAAEIKKRINDKRILETVEKWSPEINKALKSYFSVAGSKLDLYGADFGW
GKARQEILSIDGEKYAMTLCKARDFEGGLEVCLSLPKDKMDAFAAYFSLGING*
GKARQEILSIDGEKYAMTLCKARDFEGGLEVCLSLPKDKMDAFAAYFSLGING*
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Pred. No. 1.1e-145;
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complete cds.
AB010708
AB010708.1 GI:418:
Anthocyanin 5-aroma
2 (Sice, Fujiwara, H.,
                                 Submitted (22-JAN-1998) to the DDBJ/EMBL/GenBank databases. Hiroyuki Fujiwara, Suntory LTD., Inst. of Fundamental Research; 1-1, Wakayamadai, Shamamoto-cho, Osaka 618-0024, Japan (E-mail:Hiroyuki Fujiwara@suntory.co.jp, Tel:+81-75-962-8807, Fax:+81-75-962-8262)
                                                                                                      Fujiwara, H., Tana)
Direct Submission
                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Gentianaae; Gentianales; Gentianaceae; Gentiana.
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1 (bases 1 to 1679)
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for Anthocyanin
        Yonekura-Sakakibara,K.,
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                                                       TTTGTAGGGTTTATGAAGAGTTGGGCTTCCATCACTAAATTCGGAGGAGATGATGAATTC
                                                                                                             CCTAACCGTGGCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGT
                                                                                                                                                   CCCGGTCGCGGGGTGTGCATCGGAATAACGACGCACCACCGTTAGCGATGCTCCATCG
                                                                                                                                                                                         ATAAGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTT
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SLLEYDFPYPRTHFLDTYIPNIKASLSITLKHYVPLSGNLMPIKSGEMPKFQYSKDE
GDSITLLVAESDQDFDYLKGHQLVDSNDLHGLEYVMPRYIRTMCDYKYLIPLAVQVTV
FPNRGIAVALTAHBIADAKSEVMFINAMAYINKFGKDADLLSANLLPSEFDRSIIKDL
YGLEETTWNEMQDYLEMFSRGSKPPRNWAYINKFGKDADLLSANLLPSEFDRSIIKDL
YGLEETTWNEMQDYLEMFSRGSKPPRNDEMELEKFSTADCRGLLTPPCPPPWI
IRVTTFTMICGYWTTCWKISKDDVVSEESSNDENELEKFSTADCRGLLTPPCPPPWI
GNCLASCVAKATHKELVGDKGLLVAVAAIGEAIEKRLHNEKGYLADAKTWLSESNGIP
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KIHMDAFAKIFEEGFCSLS"
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/product="Anthocyanin 5-aromatic
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/db_xref="GI:4185599"
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/db_xref="taxon:55190"
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Pred. No. 1.9e-29;
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E12753.1 GI:3251585
JP 1997070290-A/1.
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Ashikari, T., Tanaka, Y., Fujiwara, H., Nakao, M., Fukui, Y.
Yonekura, K., Mizutani, M. and Kusumi, T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070290-A 1 18-MAR-1997;
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PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJUWARA HIROYUKI,
MASHIRO, MASHIKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI
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Senecio cruentus mRNA
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JP 1997070290-A/5.
  Patent: JP 1
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Ashikari, T., Tanaka, Y., Fujiwara, H., Nakao, M.,
Yonekura, K., Mizutani, M. and Kusumi, T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER
Patent: JP 1997070290-A 5 18-MAR-1997;
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PF 30-JAN-1996 JP 1996046534

PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 1:
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI,
MASAHIRO,
PI FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Ashikari,T. Tanaka,Y., Fujiwara,H., Nakao,M., Nakao,M., Fujiwara,H., Nakao,M., Nakao,M., Nakao,M., Fujiwara,H., Nakao,M., Nakao,
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PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 1
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI,
MASAHIRO,
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10,
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                                     ACGATTATGGAGTCTGTCGGAGATCATCCGCATTCCGCTCATAAATACTACTGCTTTGCC
                                                                                           GTAGATTCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTA
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2 (bases 1 to 1622)
Tanaka,Y. and Yonekura-Sakakibara,K.
Direct Submission
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/product="acyltransferase homolog"
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/protein_id="BAA93452.1"
/db_xref="aci;741559;
/db_xref="aci;741559;
/translation="magnsedikvlexcrvapppDavaeFTvpLsFedmrwlisDaeH
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TCGCGGGGTGTGCATCGGAATAACGACGCACCACCGTTAGCGATGCTCCATCGTTTGT
                                                 CGACTCAGCAGC-----AGTCGTGTCGTGTCGTTTCAAGTCACGTTATTTCCAAA 34820
                                                                                  CGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGG 461
                                                                                                                   AAAAGAACCTTTCTCCTCCACCGAGTTACACCCCATTAGTCCCGGAGTTACAAAACTCCGA 34775
                                                                                                                                                                                                                                                        CGCCGGCCATATCATCT---GGGAACCACATGATCCAAAACCGAAAATCGTCTACACCCA 34655
                                                                                                                                                                                                                                                                                           TTCATGCAATCTAATCTACCCTCTATCGCCGGAGAAAATGCCGGAGTTCCGGTATCAGAA
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Submitted (18 AUG-1998) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory
Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
(E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
Fax:+81-438-52-3934)
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                                                                                                                                                                                                                                                                                            Direct Submission

Submitted (15-JUL-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
7 (bases 1 to 101176)
Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, O.,
Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,
Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
                                                                                                                                                                             Submitted (19-JUL-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
6 (bases 1 to 1011/6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 (bases 1 to 101176)

5 (bases 1 to 101176)

Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,

Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,

Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,

Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,

Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, S.,

Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,

Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,

Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
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Submitted (13-07-1997) Arabidopsis thaliana Genome Cente:
Department of Biology, University of Pennsylvania, 38th S:
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sj
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 101176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thale cress.
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                                                                                                                                                            15, 2000 this sequence
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                                                   /organism="Arabidopsis
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 to 101176)
/clone="F21B7"
                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:9211167
                                                                                                                                                                 version
                                                                                                                                                               replaced
                                                                                                                                                                 gi:2618677
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38th Street
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e; eurosids II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="Aaf66540.1"

//brotein_id="Aaf66540.1"

//brotein_id="Aaf66540.1"

//brotein_id="Aaf66540.1"

//translation="MGHDSFCYLIVLRCALRCGIIALMOICALOKKERRSKMESSDRS
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SMDLISRRSVYEKIGDAAERWGFGVVVHGISVEVMERWKEGIERFHEQDPEVKRRFY
SRDHTRDVLYYSNIDLHTCNKAANWRDSLACYMAPDPPKLQDLPAVCGEIMMEYSKQL
MTLGEFLFELLSEALGLNPNHLKDMGCAKSHIMFGQYYPPGPOPDLTLGISKHTDFSF
ITILLQDNIGGLQVTHDQCWYDVSPVFGALVINIGDLLQLISNDKFISAEHRVIANGS
SEPRISMPCFVSTFMKPNPRIYGPIKELLSEQNPAKYRDLTIFESNTFRSQTIKITE
IPALFRATPATLASLKSPPPPKHLTIPTVDLKGASVVEKIGEAAEKWGLFHLVNHGIP
VEVLERMIQGIRGFHEDGEPEAKKRFYSHDHTRDVLYFSHNDLQNSEAASWRDTLGCYT
ABEPDDET ENI DAVGGETMIE FVETETMGIGENFER TENTOTIGGYT
                                                                                                                                                                                                                                                                                                                                                                    APEPPRLEDLPAVCGEIMLEYSKEIMSI.GERLFELLSEALGLNSHHLKDMDCAKSOYM
VGGHYPPCPOPDLTIGINKHTDISFLTYLLODNVGGLQVFHEQYWIDVTPVPGALVIN
IGDFLQVKKIMLLLRSCFISCMIWGLIILFYCVQLITNDKFISAEHRVIANGSSEPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(6700. .7357,7482.8920. .9241,9758. .10380))
/note="unknown protein; similar gb|T21964.1, and gb|AW004462.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="masciqelhfthlhipytinoqftvhpssptpanosphhslyls nlddiigarvetpsvvtypstnnresfylkrlqdalsevlypyyplsgrlrevengkl evffgeeggvlmvsanssmdladlgdltvpnramlplifrnpeegaykilempliiaq vtffgeeggvlmvsanssmdladlgdltvpnramlplifrnpeegaykilempliiaq vtffgeeggslgirlcicofgeampflgswaataktgkladpepymdretryprn ppmvkyphheylpieersnltmslmptxplqkcyriskeeggrvsladpepydeeptylcs tfdamaahiwrswykaldykpldynlruffsvnvrtrletlklrkgfygnvvclacam syveslindslskttrldyaalrvsbylrsmvdyvdvkrpkrlefggkltitqwtr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFSQQSGWVAIISSKGTCHIFVLNSSGSDAAFQPCEGEEPTRLPASSLPWWFTQSLSS
NQQSLSPPTAVALSVVSRIKYSSFGWLNTVSNATTAATGKVFVPSGAVAAVFHKSVTH
DLQLNSRTNALEHILVTTPSGHVVQHELLPSVCTESPENGLRVQKTSHVQVQEDDLRV
KVEPLOWMDVCRRSDWLETEERLPKSITEKQYDLETVSNHLTSHEDACLSLDMNSHFS
EDKYLKSCSEKSPERSHCYLSNEEVKYTSGMLPVWQNSKISHYMDSFRDSSTGGEF
EIEKVPAHELEIKQKKLLPVFDHFHSTKATLEDRFSMKCYHTSATGSHQVNGKICQDI
INCHSKPGSIESAESSEEGSTQMENLHDSDHMSNSIKSSLPLYPTVNGIYKEIEKNN
                                                                                                                         /product="F21B7.4"
                                                                                                                                                    /evidence-not_experimental
                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                 SVAIVFSTFMRAYSRVYGPIKDLLSAENPAKYRDCTLTEFSTIFSSKTLDAPKLHHFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEMYETADFGWGKPVYAGPIDLRPTPQVCVLLPQGGVESGNDQSMVVCLCLPPTAVHT
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ARDGSSDSKAGDAINYPTTVRRYSLRSHSYVVYURFRSSVCMIRCSSRVVAVGLANQI
YCVDALTLENKESVLIY PVPOPVPQGTTRVNVGYRGAYGFRMAYGFRALSKSGMYMKTGR
LSPQTTTSSPSLSPSSSGGSSFMARYAMESSKGLANGLINGDMGYKTLSKYCQDML
PDGSTSPASPNAIMKVGGVSGSDAENAGMVAVKDLVSGALVSOFKAHTSPISALCFDP
SGTLLVTASVCGNNINVFQIMPSRSHNAPGDLSYEWESSHVHLFKLHRGITSAIVQDI
                                              /protein_id="AAF86509.1"
/db_xref="GI:9280640"
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/product="F21B7.3"
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/protein_id="AAF86541.1"
/db_xref="GI:9280672"
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KAVADPKEEHLKKKLDEVTNYHHLNVNNNNTEKLQGDKMVNSQVLNAFGVCILYKDFL
translation="mrgfssvsswlwrsveigevflgstrwldavavaedavdwwvfs"
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/note="unknown protein; similar to ESTs dbj|AV529515.1,dbj|AV529566.1, dbj|AV524960.1, dbj|AV523761.1,dbj|AV523761.1,dbj|AV523761.1,dbj|AV5246743.1"
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/db_xref="GI:9280639"
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.3274,3483. .3610,3725. .41
                                                                                                                                                                                                                               protein;
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                                                                                                                                                                                                                               EST emb|Z30724.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3032,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                              37271 AACATCATCGAGACCTGTCACATCTCTCCCCCAAAGGGCACCGTTGCATCCACCACTCTT 37330
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                                                                                                                                                                                                                                                                                                                                        67
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                                                                                                                                                                                                                                                                                                                                                                                                                              7 ACCCTCCTCGAATCCTCCGAGTGGCGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTC 66
TCCTTATCTCTAACCCTCAAACACTTCTTCCCCCCTTTCATGCAATCTAATCTACCCTCTA 246
                                                                                                                                                                                                           TACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAA 186
                                                                                                                                                                                                                                                                                CCTCTCACCTTCTTCGATGCCCCCTGGCTCTCTCTCTCCCCACTCGCCGATTCTCTTCTTC
                                                                          TCCCTCTCCATCACTCTCCAACATTTCTTCCCTTACGCCGGTAAACTGATTATCCCGCCT 37510
                                                                                                                                                                             TTCTCTTACCAAAACTCAACTGAATCTTTCCTCCAAGACTTTGTACCCAACCTCAAACAT
                                                                                                                                                                                                                                                                                                           CCGCTCACCTTCGTCGACATGACGTGGCTGCATTTCCACCCCATGCTTCAGCTTCTCTTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="F21B7.;"
/protein_id="AAF86539.1"
/protein_id="AAF86539.1"
/db_xref="G1:9280670"
/tabslation="Mefkkferrslnficlpklkecargoilgykmetkaigfhhlsp-
PONIVCGHTLTAVFVNNSHQLILFGGSTTAVANHNSSLPEISLDGVTNSVHSFDVLTR
KWTRLMPIGDVPSPRACHAAALYGTLILIQGGIGPSGPSDGDVYMLDMTNNKWIKFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement()oin(18462...18515,18612...18742,18840....1897
19064...19139,19214...19410,19452....15595,19668...19752,
19865...20103,20179...20253,20345...20649,20798...20902,
21088...21216,21356...21437,21513....21608,21780....21849,
21929....22025,22408...22502,22586....22659,22810....22888,
23041....23101,23206....23315,23411....23556))
//note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGETPSPRYGHVMDIÄÄQRWLVIFSGNNGNEILDDTWALDTRGPFSWDRLNPSGNOPS
GRMYASGSSREDGIFLLCGGIDHSGVTLGDTYGLKMDSDNVWTPVPAVAPSPRYQHTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MRFTKLVWCLMFILREGFFTEAILDPVDFLALQAIRKSLDDLPG SKFTESWDFTSDPCGFAGVYCNGDKYISLNLGDPRAGSPGLSGRIDPAIGKLSALTEL SIVEGRIMGALPATISQLKDLEFLAISRNFISGEIPASLGEVGLRTLDLSYNQLTGT ISPSIGSLPELSNLILCHNHLTGSIPPFLSOTLTRIDLKRNSLTGSISPSLOPSLQY LSLAWNQLTGSVYHVLLRLNQLNYLDLSLNRFTGTIPARVFAFPITNLOPARFFFGL IQPANQUTISTVDLSYNRFEGGISPLLSSVENLYLNSNRFTGEVPASFVERLLSANIQ
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/product="F2187.6"
/protein_id="AAF86511.1"
/db_xref="GI:9280642"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESTs gb|AI993651.1,
dbj|AV538995.1*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="inttivvaqlqrqfqdyivslyqqgfidnqfselrklqdegtpdf
vaevvslffddcsklntmsisierpdnvdfkgvbggvhqlkgsssslcfvlsvqarr
Vknvcisfrecdvqnregyssnstymcdndumhrclrclqqvdyeykmlktklqdlf
Nysfklcenllylllekqilqaggtipqvdin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to protein kinase pir||A57676; similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(11965. .12033,12173. .12303,12448. .12519,12596. .12685,
12756. .12915,12985. .13041)
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AWKCVVVLRGWGLDQIGWRSVGNWVFSVRFVAGPASSLVRDLRQDSYTSANDLVPVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/db_xref="GI:9280641"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="F21B7
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                                                   GAGGAATTGCAAGCTTTTGATGATTATTTTGCGGAGGGAATAAAG
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Arabidopsis thaliana complete sequence.
AC003027
AC003027.1 GI:4079614
                                                                                                Genes with similarity to proteins in the databases are described as putative, '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANN.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genmic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (30-JAN-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buchler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Torlumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 119914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Dec 30, 1998 this sequence version replaced gi:2734094. Bases 1-9262 of clone F21M11 overlap with bases 68998-78259 of 'TAMU' BAC clone F20D22 (AC002411) and bases 119525-119914 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-OCT-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                     e-mail for correspondence: arab@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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/cultivar="Columbia"
              /organism="Arabidopsis
                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to 119914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
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genomic sequence,
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clone

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /COGO__Start=1
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/COGO__Start=1
/COGO__Start=1
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SEHKVALASVELASSTGGEAKICLSPAFATGETTNLHLPSNEDLRTAMDEKSCASIGS
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ECSISGDGWKAISNMKDITAGEENVELPWAVEINEKYPSRFRYMPHSFVFODAPVLFS
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DSLHNPTKEVYTQDIGDKTEEIDSKLRRSNUTVRDGNHYDGQGVLNPVENLIQWKSAK
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LAVDASLSTWLSTSESGSECNSASWYTLTPEKLKSTSCYSKPLRINHDDRPVLCALTL
                                                                             complement(16835. .20238
/gene="F21M11.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F21M11.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Similar to acid phosphatase; Location of ESTs
110C2T7 , gb|T42036, and 110C2XP, gb|AI100245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        усинцизові. .13488,13717. .13926,14139. .14316)
/gene="F21M11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F21M11.2"
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RDIEAMEELAWDYGIDFNDNDSLMKPFDCLCGSRFCRNKKRSTKTMQILNKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F21M11.2"
13033. .14514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8458. 18728.8875. .8027,8122. .8160,8250. .8381
10501. .10551,10685. .9893,10003. .10256,10344. .10410,
//gene="F21M11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Hypothetical protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F21M11.1"
join(7684. .7866,7965.
8458. .8728,8875. .989:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Proteins in this region are annotated in the F21M11 entry, AC002411."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="I"
/clone="F21M11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db_xref="taxon:3702"
ent(join(16835. .17185,17274. .17392,17491. .176
.17885,17982. .18079,18175. .18361,18504. .18604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overlap with bases 68998-78259 of 'IGF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .13488,13717. .13926,14139. .14514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .15831,15906. .16006,
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Matches 617
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mRNA gene

CDS gene

gene

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131 AACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCT 190
                                                                                      TCCTCGAATCCTCCGAGTGGCGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTCCCGC 70
                                                                                                                                                                                                          TCATCGAGACCTGTCACATCTCTCCCCCAAAGGGCACCGTTCCATCAACCACTCTTCCTC 48016
                                                                                                                                                                                                                                                                                                                                                          al Similarity 44.9 617; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Unknown protein; Location of ESTs 203124T7, gb|H76794 and 203124XP, gb|AA605510"
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/db_xref-"GI:4204289"
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NAGPITGDETVPYHSLSWCKNWLGFRVNITMAPQILIGKIKQQPEHDGSDVHVELNVD
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27777. 28721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F21M11.6"
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FESSYDAAHTPBSYTEQDAKKNRDITASEQPSNAARRRICGDSFIQESSPAPKTOOP
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MDYEDFLLLCPARSSVKEPNEKSGHRVSRAEBLPKINPAELCSLEQTPAFTKELVLGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Join(20752. .20994,21362. .21497,21596. .21740,21825. .21
22102. .22178,22542. .22758,22920. .23064,23343. .23442,
23599. .23693,24021. .24072,24227. .24298,24441. .24647)
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20752. 24647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Hypothetical protein"
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/db_xref="GI:4204287"
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                                                                                                                                                                                                                                                                                                                                                                                 5.8%;
44.9%;
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20188. .20238))
                                                                                                                                                                                                                                                                                                                                          Score 87.8; DB 7;
Pred. No. 7.3e-08;
0; Mismatches 717;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 119914;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCGGGGAACTACTTCGGAAACTGTCTATCGTTTGCGATGGCGAAGATCCTGCGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTCTGAGAATCAATCTCCTGTTTTCTACCTTCGTGGTGACTCTAGCTTTCATTTGGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCCACTTTTACATTGAGCCGGAAGCAGATAGATAATCTAAAAAGTTGGGTTACAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTTTGGAGCCAAAACTCTGCAAAACACAGTTCACATGTTACGCCTGAGAACATGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCACAGCTGCAGAAACATGATCAAGGACCCAGGCGAGGTAGGCGCAGGACATTTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCATTGACCAAATCCAGCGGTAAAGATCCCGCCACGGTTCTTCTACCCTCTCTGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTCAGCTACACATGTTGTAGCAGATGGAGTCACCTTCAGTCATTTCATGAAGTATTGGA
CGGATTTTGGATGGGGTAAGGCGTGAAGCAAGAGATACTGTCGATTGATGGAGAGAAGT
                                                       GGGTCATGTCCCATTATCCAACCTCAATTGCAGGAGCTCCGAAATTGGGACTGTATGACA
                                                                                                                 AAGCCTTGCAAAACTGTTATTTCTCGGTGGCGGGATCGAGCAGGCTTGATCTTTACGGCG
                                                                                                                                                                                                                                                                                            ATTTGCTAGGAGAAAAATGCGTTTTGGCGGCTTCAGATGCAATCACAGCGAGAATCAAAG
                                                                                                                                                                                                                                                                                                                                ATTTGGTCGGAGATGAAGGGGTGTTTCGGGCAGCTGAGGCGATCGCGGCGGCGGAAATAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                             TACCACAAACATACTTTGGCAACTGTATGGCTCCTGGTATCGTATCAGTCAAGAAACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTATTTCACTTGATGATCAATGTGGATTGCAGGAATCGCCTCAAGTACACAACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTGATCAAGACACTTGTACAAGACAGTGAAACAAAGGCCAACGAGGAAGACAAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCTACCTACCTTTTCACCCAATCTGAAATTAAGAAATTGAAGGGTTTGATTCAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCCATCACTAAATTCGGAGGAGATGATGAATTCTTGGACGGAAAAGGTGAATGTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATCTCTAACCCTCAAACACTTCTTCCCCCCTTTCATGCAATCTAATCTACCCTCTATCGC
                                                                                                                                                                           ATATGTTATCAAGCGATCTGTTGAAGACAGCACCAAGATGGGGGACAAGGAGTACGTAAAT
                                                                                                                                                                                                                                  AGAGGACGAGCGACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGAGATTCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGCGCTTTCTTTTAATTCCGATCGATTTAAGGCCGCGTTTGGAT-----CCGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATCGCCAAATCGGTCGGAGATTA--------CAAAGACGTGGATGACGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCCCCAAATGTAGTTAATCTCTTCCTTCGTCGCGATCGCAGCTTATATCTGGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGCGCAGAAACGTCCGTTGGAATCGCAGCATCCATCTTTACCGACGGATCGGATTC---
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Submitted (09-JUN-1999) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
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                                                                                                                                                                                                                                                                                                                               Submitted (01-JUN-2000) The Institute for Genomic Research, 9 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org On Jul 28, 2000 this sequence version replaced gl:9440543.

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATTATTTTGCGGAGGGAATAAAGGGTTGATTAATCATTTTAATCATGTATTATGAAGTTG
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RESULT 13
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Direct Submission
Submitted (13-OCT-1999) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (B-mail:ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/gene-s2/, Tel:81-438-52-3935, Fax:81-438-52-3934)
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                                                                                                                                                                                                                  Nakamura,Y.
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              Submitted (20-JUL-2000) The Institute for Genomic Research, 9 Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.org * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                              Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Koo,H., Fujii,C.Y., Utterback,T., Barnstead,M.E., Bc White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana 'IGF' BAC 'F2789' genomic seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana chromosome ? clone IN PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                Town, C.D. and Kaul, S.
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1 (bases 1 to 166884)
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/strain="Columbia"
/db_xref="taxon:3702"
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*** SEQUENCING
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CB10 15Å, UK
On Aug 12, 1999 this sequence version replaced gi:5531400.
For more information about this sequence or the Malaria Project,
                                                                                                                                                                                                                                                                                              PFMAL4P4 224448 bp DNA HTG Plasmodium falciparum chromosome 4 strain 3D7,
                                                       The Sanger
                                                                           Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium,
                                                                                            Direct Submission
                                                                                                                                                                                  Plasmodium falciparum
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                                                                                                               and Barrell,B.
                                                                                                                                 Bowman,S.,
                                                                                                                                                                                                       malaria parasite P. falciparum
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/db_xref="taxon:3702"
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44842: contig of 7162 bp in length
44892: gap of unknown length
69074: contig of 24182 bp in length
69124: gap of unknown length
135012: contig of 65888 bp in length
135012: gap of unknown length
135062: gap of unknown length
159445: contig of 24383 bp in length
159459: gap of unknown length
159459: gap of unknown length
166884: contig of 7389 bp in length.
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4.3%; Score 65.8; D3 71; Length 224448;
Best Local Similarity 62.4%; Pred. No. 0.0023;
Matches 103; Conservative 0; Mismatches 62; Indels 0;
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Order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working draft' seguence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, because the sequence with foreign sequence from E.coli, yeast, vector,
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/chromosome="4"
23258 c 21957 g 75240 t 23201 others
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/strain="3D7"
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Ashikari T, Fujiwara H,

Fukui Y,

Kusumi T,

Mizutani M;

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ALIGNMENTS

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RESULT
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17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                                        Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                CDS
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                                                                                                         WO9625500-A1.
                                                                                                                                                                                                                                                                                               T37313 standard; cDNA to mRNA; 1518
                                                                       16-FEB-1996;
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CTTTTTTGAGTCAATAAAAAAAAAAAAAAAAAAAAAAATGAAAAAACTCAGTTATTTT
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Matches 1056
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17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                            Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 65-69; 94pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA coding for aromatic acyl transferase - which produce anthocyanin pigments and thus e.g. of flowers
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Scenecio cruentus;
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cagaatctagcgacgacttcgatgatctcgtcggaaatcgtccagaatctcccgttaggc
                       TGGAGTCTGTCGGAGATCATCCGCATTCCGCTCATAAA;ACTACTGCTTTGCCCCTAGCG
                                                              CCTTATCCTCTAACCCTCAAACACTTCTTCCCCCCTTTCATGCAATCTAATCTACCCTCTAT
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Pred. No. 9.6e-138;
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       gtaacaattaattaagtgttgagtaacgtgaagaataatccctattatatattatgatt
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17-FEB-1995;
29-JUN-1995;
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                                                                                                                                                                                                                             Claim
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Local Similarity
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                 CCCATGCTTCAGCTTCTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACC
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   Query Match
Best Local Similarity
Matches 730; Conserv
                                                                                      Vectors containing DNA fragments encoding proteins of plant original with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                            30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                                                                                                                                                        Ashikari T, ruj.
                                                                                                                                                                                              Claim 4; Page 69-72;
                                                                                                                                                                                                                      DNA coding for aromatic acyl transferase - which produce anthocyanin pigments and thus e.g. of flowers
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Gentiana triflora; Petunia hybrida; Perilla
Scenecio cruentus; Lavandula angustifolia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in cotone changes and allowing new colourations to be produced. Sispecific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA coding for aromatic acyl transferase - which produce anthocyanin pigments and thus e.g. of flowers
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Nakao M, Tanaka Y, Yonekura K;
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                                                            CCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCTAAATTGGACACATATTTATGGAAC
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                                           cctatgtacgacagatctgtggtgcaagatccatttcatattcgtcgaaaaatctacaat
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AACGCGCAGAAACGTCCGTTGGAATC-----GCAGCATCCATCTTTACCGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes a human LOBO protein described in the method of the invention.
                                                                                                                                                                                                                                                      diagnostic; pharmaceutical; gene spondyloepiphysal dysplasia; acho
                                                                                                                                                                                                                                                          LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-601320/51.
                                                                                                                                                07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                            Z23902;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Z23902 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-1998;
Rosenthal A,
                                                                         27-MAR-1998;
                                                                                                                                                                                     WO9950284-A2
                                                                                                                                                                                                                                                                                                                                 Human LOBO homologue genomic
                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                  (ROSE/) ROSENTHAL
                                                                                                           26-MAR-1999;
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTTTTT 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCTGTTTCATCTCTATTGTTTAAACAATAATTTTTTTCCATTGAACTTTTTTGAGTCA 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 4.1%;
1 Similarity 68.0%;
87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acids encoding properties and for treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49999
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                                                                                                                                                                                                                                                                                                                                                                      (first entry)
Rump
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                           99WO-EP02055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 49999
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Pred. No. 0.0023;
0; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                 DNA fragment
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disorders
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 Wirth
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RESULT 8
Q27886/c
ID Q27886;
XX
Q27886;
XX

DT 04-FEB-1993 (first ent
XX
Polymerase chain reacti
XX
FI
KW Plasmodium falciparum;
XX
Synthetic.
FH Key 1670-95
FT - /*tag-
FT exon 1111.2
FT repeat_region 1249.2
FT repeat_region 1249.2
FT PN EP499834-A.
XX
PF 26-AUG-1992.
XX
PF 27-JAN-1992; 92EP-010
XX
PF 27-JAN-1992; 91DE-410
XX
PR 21-FEB-1991; 91DE-410
XX
PA (BEHW ) BEHRINGWERKE AG
XX
PH Hundt E, Knapp B, Kup
XX
Hundt E, Knapp B, Kup
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PH Hundt E, Knapp B, Kup
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The method and nucleic acid molecules, etc. are useful for production of transgenia animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes a human LOBO protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 49999
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                                                                                                                                                                                                                                                                                                                                                                                              chain reaction; glycophorin binding protein; inverse PCR; falciparum; malaria; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 300-328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.6%;
ilarity 84.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                            91DE-4105348
                                                                                                                          92EP-0101271
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/number= 1
1111..2202
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/*tag= c
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767..955
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                                Kupper H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compounds e.g. for gene therapy. The method etc. are useful for production of transgenic
                                  Nolte
                                'n
                                Kuepper
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RESULT 9
N90703/c
ID N90703:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycophorin binding protein 130h is a P.falciparum blood stage antigen 69% homologous with the known GBP130. The GBP130h gene and its homologues can be used in vaccines to protect against malaria caused by P.falciparum. The coding sequence was isolated using PCI techniques on a genomic P.falciparum FCBR strain library. The GBP130h gene was found to be highly conserved between different Strains but is distinct from the GBP130 gene.
                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1332 TTTTGCGGAGGGAATAAAGGGTTGATTAATCATTTAATCATGTATTATGAAGTTGGATGA 1391
Rhoptry membrane antigen
                   WPI; 1989-263714/36 P-PSDB; P91632.
                                                                                          12-FEB-1988;
                                                                                                              10-FEB-1989;
                                                                                                                                 24-AUG-1989.
                                                                                                                                                     W08907645-A
                                                                                                                                                                                                               Plasmodium
                                                                                                                                                                                                                                   Malaria;
                                                                                                                                                                                                                                                     Rhoptry membrane antigen-1 gene
                                                                                                                                                                                                                                                                           25-JAN-1990
                                                                                                                                                                                                                                                                                               N90703;
                                                                                                                                                                                                                                                                                                                                                                                      1512 TTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2418 BP; 1047 A; 303 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 12-14; 17pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA coding protein GBP 130 h and
                                                                     (SARA)
                                                                                                                                                                                                                                                                                                                                                                   586 TAATTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                          706
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                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                      SARAMANE PTY LTD
                                                  ğ,
                                                                                                                                                                                                                                   rhoptry membrane antigen-1; antibodies
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                                                  Crewther
                                                                                          88AU-0006743
                                                                                                              89WO-AU00056
                                                                                                                                                                       Location/Qualifiers 634..2202 /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                      1522
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                                                                                                                                                                                                                                                                                                                   2662
                                                  PΕ,
of Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                  Smythe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 13
Pred. No. 0.038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 G;
                                                  JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               776 T; 0
                                                  Marshall VM,
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0,

SXX CCC CXXX PF

Claim 8; fig

1; 46pp; English.

used for producing antibodies and in immunisation, diagnostic and treatment methods for malaria.

The RMA-1 gene can generate an immune response to malaria, antibodies which can inhibit growth of the parasite. RMA-1 has mol. wt. 80 kD.

and initially

Sequence 2662 BP; 1134 A; 307 C; 387 G; 834 T; 0 other;

Matches Query Match Best Local

84; Similarity

Conservative

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3.5%;

Score 54; DB; Pred. No. 0.06; 0; Mismatches

0.06; , 10; 50;

Length 2662; Indels

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0,

Local

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RESULT 11
011712/c
ID 011712 standard; DNA; 3138 BP.
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Shuttle vector pMUW1630 was constructed for use in E. coli and transfer back into Dictyostelium. It includes a fragment of the Dictyostelium plasmid Ddp2 containing the origin of replication, encoding the secretion signal peptide of the D19 gene, a sequence PsA, Actin 15 polyA signal and an ampicilline resistance conferring sequence. See also Q11710 and Q11711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                გვგვგვჯჯ
                                                                                                               Polypeptide facilitating extra-chromosomal replication -recombinant plasmid in Dictyostelium species
                                                                                                    Claim 35; Fig 15; 90pp;
                                                                                                                                                           WPI; 1991-164194/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local (
                                                                                                                                                                                                      (UYMA-) MACQUARIE UNIV.
                                                                                                                                                                                                                             02-NOV-1989;
                                                                                                                                                                                                                                                     02-NOV-1990;
                                                                                                                                                                                                                                                                            16-MAY-1991.
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                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum.
                                                                                                                                                                                                                                                                                                                                                                                              slime mould; replication;
                                                                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                    Shuttle vector pMUW1630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q11712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1763 acaacttcatttatatacaggcttcccttttttatttttaaaggatacgtttcacttaat 1822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primers and probes which may be used in the diagnosis of viral, bacterial or fungal infections, allergic responses; hereditary disease, lymphoma or carcinoma or other conditions which activate genes of the lymphoid tissue. Inhibitors of HEDG, e.g. HEDG-specific antibodies, can be used to treat inflammation or disease as described above. Inhibitors of HEDG are also useful for controlling signal transduction in rheumatoid synovium (from where it is derived)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1875 BP; 478 A; 477 C; 410 G; 510 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ottttaaaagattttgtgtggtttggtgcaagtcagaataaattctggctagttgaatcc 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTTGATGATTATTTTTGCGGAGGGAATAAAGGGTTGATTAATCATTTAATCATGTATTA 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97;
                                                                                                                                                                               Chang ACM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                           89AU-0007187.
                                                                                                                                                                                                                                                 90WO-AU00530
                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "finish position
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
2068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%;
56.7%;
                                                                                                   English.
                                                                                                                                                                                Williams
                                                                                                                                                                                                                                                                                                                                                                                           Rep gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52.6; DB Pred. No. 0.11; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         Ddp2;
                                                                                                                                                                                                                                                                                                            not given'
                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
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                                                                                                                            of.
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CCCXX STATE OF STATE

W09700952-A2

EDG-2; rheumatoid synovium; G-protein linked; seven pass; infection; bacterial; viral; fungal; allergy; lymphoma; carcinoma; cancer; neoplasia; lymphocyte; leucocyte trafficking; ss.

EDG-2 receptor homologue (HEDG) cDNA sequence.

Homo sapiens

Location/Qualifiers 309..1403

29-APR-1997 T48669;

(first entry)

T48669 standard;

cDNA; 1875

ВP

10

T48669 is a cDNA sequence encoding homologue, HEDG. The cDNA sequence

the

human EDG-2 be used for

receptor the production

of

Claim 2; Page 25; 35pp; English.

New isolated human EDG-2 receptor homologue - used to develop prods for the diagnosis or treatment of inflammation or diseases which activate genes of lymphoid tissues.

WPI; 1997-087379/08. P-PSDB; W10879.

Au-young J,

Bandman o,

Coleman

₩,

Guegler KJ,

Seilhamer

PHARM INC. 950S-0567817. 950S-0000352.

06-DEC-1995; 20-JUN-1995; (INCY-) INCYTE

20-JUN-1996;

96WO-US10618

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168

TTTTTTTTTTTT 155

1508 TTTTTTTTTTTTT 1521

ATAAATTAGGTTTTTAAAATTATATTAAAATAAAAAAATATATTACAATTTATATTCT

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RESULT 12
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Best Local S
Matches 88
Query Match
Best Local Similarity
                                                          clag genetic species, and the products encoded by them, enables range of therapeutic agents to be rationally designed and/or identified that are useful for the prophylaxis and treatment of disease conditions caused or exacerbated by infection with plasmodium spp., e.g. malaria, especially in humans.
                                                                                                               This is the nucleotide sequence of a clag9 paralogue gene on chromosome 3 of Plasmodium falciparum. It is a paralogue of the newly identified cytoadherence linked asexual gene 9 (clag9) on chromosome 9 of P. falciparum. The clag9 gene encodes a protein (see Y31945) that facilitates cytoadherence of erythrocytes parasitised with Plasmodium to other cells. The identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1432
                                                                                                                                                                                                            New proteins useful especially malaria
                                                                                                                                                                                                                                                                                                                                                                                                                            Clag9; paralogue; cytoadherence linked asexual gene; CLAG; erythrocyte; red blood cell; malaria; infection; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1492
                                          Sequence 8365
                                                                                                                                                                                          Disclosure; Page 85-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1372
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                                                                                                                                                                                                                                              WPI; 1999-591099/50
                                                                                                                                                                                                                                                                  Kemp
                                                                                                                                                                                                                                                                                                            25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                     30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                         W09949048-A1
                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88;
                                                                                                                                                                                                                                                                                      MENZIES SCHOOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                          BP;
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                                         3570 A; 931 C; 981 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.48;
                                                                                                                                                                                                                                                                  KR,
                                                                                                                                                                                                                       for treatment of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
 S G
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                                                                                                                                                                                                                                                                                      HEALTH
. 48;
                                                                                                                                                                                        150pp; English.
                                                                                                                                                                                                                                                                 Gardiner DL,
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Score
Pred.
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                                                                                                                                                                                                                                                                Holt
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DB 20;
0.26;
                                         2883 T;
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                                         0 other
        Length 8365;
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                                                                                                                                                                                                                                                                 AF;
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RESULT
N90224/
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Best Local (
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antibodies, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24/c
                                                                                                                                                                                             The DNA is of a malaria-specific DNA insert of clone 41-2. The encoded peptide (see P90417) is useful in a protective vaccine, esp. against malaria. Produced antibodies are useful for passive immunisation, and antibodies, the protein and the DNA sequence are useful as diagnostic reagents. See also N90211-25 and P90403-19.
                        1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1500
                                                                                                                                                                                                                                                                                                     New antigenic proteins from Plasmodium falciparum - new encoding nucleic acid sequences and derived antibodies, useful in vaccines, diagnosis etc
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                           Claim 1; Table 17; 25pp; German.
                                                                                                                                                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                      Knapp B,
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP322712-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; malaria; clone 41-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malaria-specific DNA insert of clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N90224
                                                                                                                                                                                                                                                                                                                                                                                                               (BEHW ) BEHRINGWERKE
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                                                TCTGTTTCATCTCTATTGTTTAAACAATAATTTTTTTCCATTGAACTTTTTTGAGTCAAT 1456
                                                                                                                                                                                                                                                                                                                                               1989-194071/27.
DB; P90417.
TTTTTTTTTTTTTTTTTTTT 1522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108;
                                                                                                     Similarity 62.7 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                      1052
                                                                                                                                                                                                                                                                                                                                                                                      Hundt E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                      BP;
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                                                                                                                                                                    394 A;
                                                                                                                 3.3%;
                                                                                                                                                                                                                                                                                                                                                                                       Enders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1052
                                                                                                                                                                    93 C; 88 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                      В,
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                                                                                                     Score 50.8; DI
Pred. No. 0.21
0; Mismatches
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                                                                                                                                                                      477 T;
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                                                                                                                                                                                                                                                                                                                                                                                      Ξ
                                                                                                                 .21;
                                                                                                                                DB
                                                                                                                                                                      0 other;
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526 TGTTTT

1517

TTTTTT

1522 521

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Matches
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17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                         Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour
                                                                                                                                                                                                                                                             e.g.
                                                                                           tone changes and allowing new colourations to be produced Six specific DNA sequences encoding aromatic acryl transferase from different plants are described in T37308-T37313. NOTE: This sequence is supposed to cross reference with the protein described in w04727, however there are so many discrepanteles between the polypeptide decoded from this sequence and the polypeptide discrebed in W04727 that the indexer decided the specification and described in W04727 that the indexer decided
                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plants; acylation; colour; tone; colouration; colour change;
Gentiana triflora; Petunia hybrida; Perilla ocimoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lavandula angustifolia (Clone pLAT21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T37313 standard;
                                                                                                                                                                                                                                      Claim 4; Page 73-76; 94pp; Japanese
                                                                                                                                                                                                                                                                                                                                               Ashikari
                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9625500-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scenecio cruentus; Lavandula angustifolia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aromatic acyl transferase; transformation; anthocyanin pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aromatic acyl transferase coding sequence
                                                            Sequence 1518
                                                                                                                                                                                                                                                                           which
                                                                                                                                                                                                                                                                                                                                    Nakao
                                                                                                                                                                                                                                                                                                                                                                     (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-1996
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              Local
                                                                                                                                                                                                                                                             coding for aromatic acyl transferase - ch produce anthocyanin pigments and thus of flowers
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                                                                                                                                                                                                                                                                                                             1996-393401/39
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                                                                                    cross
                                                                                                                                                                                                                                                                                                                        Tanaka
              Similarity
                                                                                                                                                                                                                                                                                                                                              Fujiwara H,
                                                                                    reference the two.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                           96JP-0046534.
95JP-0067159.
95JP-0196915.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= Aromatic acyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                             384
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            3.3%;
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                                                            340 C;
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ura K;
Score 50; DB Pred. No. 0.32 0; Mismatches
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                                                             366 G;
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                                                             428
                        DB 17;
            .32;
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                                                             7
                                                                                                                                                                                                                                                                       for transforming altering colour
  10;
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                        Length 1518;
                                                             other;
 Indels
                                                                                                                                                                                                                                                                       plants
tone,
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1328 ATTATTTTGCGGAGGGAATAAAGGGTTGATTAATCATTTAATCATGTATTATGAAGTTGG 1387

Query Match Best Local S Matches 92

l Similarity 92; Conserv

Conservative

3.3%;

; Score 50; DB ; Pred. No. 0.38 0; Mismatches

0.38;

DB

18; 70;

Length 5173 Indels

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Gaps

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RESULT 15
T89783
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                      This cDNA sequence encodes the TRP-185 protein, a 185 kD specific cellular protein that regulates HIV gene expression by binding a transactivating RNA region (TAR) of the Human Immunodeficiency Virus long terminal repeat (HIV LTR). The structural integrity of 'TAR RNA stem, loop and bulge regions is a key element for the activation of the viral transactivating protein tat, which reportedly binds to the TAR bulge region via its basic domain. Binding of the TRP-185 to the TAR region of HIV RNA increases the transcription of wild-type HIV LTR resulting in a four-fold increase in the replication of the virus. This protein can be used to produce antigenic polypeptides which can be used to study HIV and cellular gene expression or in the preparation of immunodiagnostic agents and therapeutic agents (i.e. inhibitors) for the treatment of HIV related diseases (e.g. AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1458
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                                                                                                                                                                                                                                          DNA encoding human immunodeficiency virus binding protein TRP-185 useful to produce antibodies to diagnose or study epidemiology of acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus; HIV; transactivating region; cellular protein; long terminal repeat; LTR; tat protein; immunodiagnostic agent; therapeutic agent; TRP-185; antigen acquired immunodeficiency syndrome; AIDS; ss.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5677143-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T89783 standard;
                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                      (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1991;
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PCT-US95-07201-43
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US-08-747-2218-24
  US-08-514-014-1

US-08-833-823-1

US-08-813-150-1

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PCT-US96-10618-1

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Patent No. 5231168	Sequence 4, Appli	Sequence 1, Appli			Sequence 36, Appl	•	14,	1,	36,	1,		Sequence 2, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 19, Appl	Sequence 19, Appl	Sequence 5, Appli	Sequence 15, Appl

ALIGNMENTS

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US-08-232-463-14
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US-08-232-463-14
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                                                                                                                                                          TELEFAX: (703)683-410
TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935
FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: 606140
                              TOPOLOGY: line
IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                      LENGTH:
TYPE: n
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ZIP: 22313-0299
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STATE: VA
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1800 Diagonal Road,
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APPLICATE: 26-AUSTINE PILING DATE: 26-AUSTINE ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION:

""" FPHONE: (703)836-9300
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Best Local Similarity
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                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                             ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHBIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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CITY: Alexandria
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1800 Diagonal Road,
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GENERAL INFORMATION:
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Best Local :
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SEQUENCE CHARACTERISTICS:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
                                                                                                                                                                                                                                                                                                      APPLICANT:
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TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1147
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              PRIOR APPLICATION DATA:
                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          967 TCGTTTGCGATGGCGAAGATCCTGCGGCGGGATTTGGTCGGAGGATGAAGGGGTGTTTCGG 1026
                                                                                                                                                                                  STATE: C
COUNTRY:
                                            APPLICATION NUMBER: FILING DATE: 20-JUN
                                                                                                                                                                                                             STREET: 3174 POI
CITY: Palo Alto
                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 4.0%; Pred. No. 0.00031; ses 16; Conservative 225; Mismatches 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                    Au-Young, Janice
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                 Coleman, Roger
Guegler, Karl J.
                                                                                        FastSEQ Version 1.5
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                                            20-JUN-1996
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60/000,352
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-DEC-

20-JUN-1995 ON DATA: UMBER: 08/5 06-DEC-1995

08/567,817

FILING DATE:

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Best Local Similarity
""" hes 97; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/07867106 Patent No. 5389526
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1875 base pairs
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19920625
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                            APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
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LIBRARY: Rheum
CLONE: 80853
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REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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          APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                           ZIP: 19103
                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                          CITY: Philadelphia
STATE: PA
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02-NOV-1989
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Pred. No. 0.0019;
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                                               TELEPHONE: 713-787-14
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,7
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 5173 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gaynor, Richard B
APPLICANT: Wu, Foom W.
TITLE OF INVENTION: Cellular
TITLE OF INVENTION: and Uses
TITLE OF INVENTION: Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1372 TGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAATAATTTTT 1431
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REGISTRATION NUMBER: 35,134
REFERRNCE/DOCKET NUMBER: RIG
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-568-3100
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ANTI-SENSE: N
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                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
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; LOCATION:
US-08-242-677-1
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5198345-15
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TITLE OF INVENTION: VECTORS IN USE IN FILAMENTOUS FUNGI
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                      ; DAVIES,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5198345
                                                                                                                         SEQ ID
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Best Local Similarity
Matches 92; Conserv
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                                        Query Match
Best Local
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   1514 TTTTTTTTT 1522
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APPLICATION NUMBER: US/
FILING DATE: 20-DEC-1985
5102
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                                                                                                                                     FILING DATE:
                                                                                                                                     APPLICATION NUMBER: US/07/811,404 FILING DATE: 20-DEC-1985
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Pred. No. 0.0034;
0; Mismatches 1
                         Score 49.8; DB 7;
Pred. No. 0.0034;
0; Mismatches 12;
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Pred. No. 0.
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RESULT 9
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Best Local S
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                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1999
ATTORNEY,AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Slade,
                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4:
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APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 53895;
STREET: One Liberty Place 46th Floor
                                                                                           1859 AATGGTTTAAAAAAACTTGGGTTGGTTAATTATTATTTGAAAATTTTAAAAACCCAAATTA 1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                     DB 1;
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Sequence 2, Application US/07867106 Patent No. 5389526

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3340934-5
;PATENT NO. 5340934
; PATENT NO. 5340934
; APPLICANT: TERMINE, JOHN D.;YOUNG, MAKLAN L...
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FTI.ING DATE: 03-NOV-1989
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5340934-5
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US-07-867-106-2
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Best Local Similarity
Matches 67; Conserv
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INFORMATION FOR SEQ ID NO: 2:
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STRANDEDNESS: SI...
TOPOLOGY: linear
TOPOLOGY: DNA (genomic)
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LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
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TELEPHONE: 215-568-3100
TELEFAX: 215-568-349
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MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
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LOCATION:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RI
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APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
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FILING DATE: 19920625
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Chang, Andy C M
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2378..5038
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.013;
0; Mismatches 29;
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; CLONE: 8D4-T3
US-08-330-108-16
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5340934-5
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                                                     Query Match
Best Local S
Matches 77
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Best Local Similarity
Matches 73; Conserv
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FILING DATE:
INFORMATION FOR SEQ ID NO: 16:
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                                                                                                                                                                                                                           TOPOLOGY: 111CL.
MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                      1364 TTTAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAA 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-D
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
                                                                                                                                                            CELL TYPE: T-C
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ORGANISM: human
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                     Local Similarity
nes 77; Conserv
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                               LENGTH: 198 base pairs
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SYSTEM: PC-DOS/MS-DOS
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                                                                Score 47.6; DB 2; Pred. No. 0.012;
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PCT-US92-10087-16
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PCT-US92-10087-16
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                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-227-5941
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: no ANTI-SENSE: no
              FILING DATE: 20-NOVEMBER-1991
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: DCI-028PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: LDW ... PC-U
OPERATING SYSTEM: PC-U
ASCII TEXT
                                                                             1364 TTTAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAA 1423
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 198 base pairs
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TELEPHONE: 617-227-7400
TELEFAX: 617-227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, Kendall A.
TITLE OF INVENTION: IL-2-Stimul
TITLE OF INVENTION: Expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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  128
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                                                                                                                                                                                                                       CELL TYPE: T---'
                                                                                                                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                      LIBRARY:
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UCLEIC ACID
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                       Score 47.6; DB Pred. No. 0.012;
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                                                                                                          49;
                                                                                                                                   Length 198;
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US-07-867-106-2
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US-07-867-106-2
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                                                                                                                                                     Query Match 3.1%;
Best Local Similarity 64.8%;
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                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO: 2:
                                                                    1970
                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
                                                                                                    APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILLING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
2030 AAAAAAAAAAAACCCTCATTATAAATATTAATTACTTTGGTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                    Score 47.2; DB Pred. No. 0.048;
                                                                                                                                       Mismatches
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                          1473 AAAAAAAATGAAAAACTCAGTTATTTTTTTTTTTTTTT 1514
                                                                                                                                          1353 TIGATTAATCATTTAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTAT 1412
                                                                                  IMMEDIATE SOURCE:
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LENGTH: 860 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: Jones IIT
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Allergens of Alder Pollen
TITLE OF INVENTION: Applications Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jones III, Harry C
REGISTRATION NUMBER: 20,;
REFERENCE/DOCKET NUMBER:
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                                                      TTTTTTTTTTTTTTTTTTGCTTATAATGTATTAAGTCAACATAAACAAATTGTGCTTATG 795
INFORMATION:
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New York
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                                                                                                                                                                                                                                                                                                                                                                                                                    860 base pairs
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Kraft, Dietrich
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Pred. No. 0.031;
0; Mismatches 72; Indels
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; ORIGINAL SOURCE:
; ORGANISM: Cand
US-08-817-926-27
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US-08-817-926-27/c
                                                                                                      Query Match 3.1%;
Best Local Similarity 51.4%;
Matches 108; Conservative
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1370 CATGTATTATGAAGTTGGAAGTCGAAATCCTCTCTTTCATCTCTATTGTTTAAACAATAATTT 1429
                                   1310 AATTGCAAGCTTTTGATGATTATTTTGCGGAGGGAATAAAGGGTTGATTAATCATTTAAT 1369
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 4818 base pair
                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 081356/0112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Bent, Stephen A.
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APPLICATION NUMBER: JP 42536/1996
FILING DATE: 29-FEB-1996
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/JP96/02597 FILING DATE: 12-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 09-MAY CLASSIFICATION: 439
                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 12-SEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iwamatsu, Akihiro
Kato, No. 6001590uo
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                                                                                                                                                                                                                                                            linear
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12-SEP-1995
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09-MAY-1997
                                                                                                                                                                                                                                                                            double
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                                                                                                                                                                                                                                                                                                                                             27:
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                                                                                                      Score 46.8; DB 5;
Pred. No. 0.055;
0; Mismatches 102;
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                                                                                                                                    Length 4818;
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Title:
Perfect score:
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Maximum
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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gb_est11:
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gb_est2: *
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Compugen Ltd.
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ALIGNMENTS
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AL276226 Tetraodon
AW695291 NR093E098
AL058926 Drosophil
AL061936 Drosophil
AL097166 Drosophil
AL097431 Drosophil
AL0212733 Tetraodon
AW616119 EST296884
                                                                                                                                                                                                AW093479 EST286659
BE187619 EST336180
AW774948 EST334099
AW692527 NF056D05S
AW586972 EST318595
BE353747 EST355090
AV440958 AV440958
AL097377 Drosophil
BE323055 NF001A07P
AW56086 EST315734
AL127297 Tetraodon
AL176843 Tetraodon
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AL106003 Drosophil
AW587016 EST318639
AL175696 Tetraodon
AL188420 Tetraodon
AL064091 Drosophil
AL217379 Tetraodon
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BE434257 EST405335
AW650280 EST328734
AW616206 EST307245
AW930934 EST356777
AW038515 EST280198
                                        AL255325 Tetrac
AI297571 LP11902.
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CTTTTTTCGAGACTGATATGAATTTCAATTATCTCATTGGTGACCATCCGCGTAAGGCTA
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                                                                                                                                                                                                                                                                                                                                                       Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW221049 606 bp mRNA EST297518 tomato fruit mature green, cDNA clone cLEF3F1, mRNA sequence. AW221049 GI:6532733
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100 Jordan Hall, Clemson, SC
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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Fax: 864 656 4293
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a 143 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="tomato fruit mature green, TAMU"
/tlssue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripen
/lab_host="SOLR"
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/clone="cLEF3F1"
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Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronn
, Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon esculentum Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
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Fax: 864 656 4293
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a 140 c
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/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4081"
/clone="cLEF3F3"
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lycopersicon
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                           Score 138.6; DB 2
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                                                                                               Mismatches
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                                           Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                      Fax:
                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, I
                                                                                                                                                                                                                                                                               Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanne,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Wartin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurs,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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Glycine max
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                   Seq primer:
                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                 info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40RP from Gibco
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                                             CCAGCTGCCGCCGATAGTCGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCA
                                                                                                 CACCCTCCTCACATCAGATTCACCACAAGACGTTCCAAATTGGCACCCTCTTGTTCCCGC
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GTTTCCTACCCCACGTGTTGACCAAGATGGCGCACGTGTGTTCCCTCTTATGGCCATTCA
                                                                                                                                                    TCATCCGCATTCCGCTCATAAATACTACTGCCTTTGCCCCCTAGCGACGATTATGAAGATCT
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                                                                                                                                                                                                                                                           GTTCCGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used [GAGACAGAGAGAGAGAGAGACTAGTCTCGAG(T)-18]. After second-strand synthes is, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The xhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 400bp cutoff, using a SizeSep 400 Spun column from Pharmacia. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with ECORI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."

57 a 247 c 91 9 187 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2-month-old 'Williams' plants that were greenhouse grown in 5-gallon pots. To suppress nodulation, Black Gold All-Purpose potting soil was supplemented with: 0.36g/L available phosphoric acid (P205), 20mg/L urea N, 0.16g/L S, 0.49mg/L B, 2.5mg/L Cu, 0.15g/L Fe, 13.53mg/L MN, 0.26mg/L B, 2.5mg/L Cu, 0.15g/L Fe, 13.53mg/L MN, 0.26mg/L MO, 14mg/L Zn, 20mg/L Ca, and the following nutrients in a slow-release form (Osmocote): 0.165g/L ammonia N, 0.185g/L nitrate N, 0.35g/L available phosphoric acid, and 0.35g/L soluble potash. No nodules were visible on the roots at harvest. Stratagene's cDNA synthesis Kit (catalog #20401) was used to synthesize the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript II XR; Site_1: EcoRI;
XhoI; The mRNA was isolated from entire roots of
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE
/clone_lib="Gm-cl009"
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Pred. No. 2.1e-15;
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                               CGCCGTATGAGGCGGATATTATTTTACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAA
                                                                                                   CACCCCATGCTTCAGCTTCTCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAA 162
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 AACATTATTCCTCCTCTTAAAAATTCACTCTCCCTCACTCTCAAACACTATACGCCCTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 864 656 4366 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: David Frisch
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Llang,F. Hansen,T.S., Craven,M.B., Bowman,C.L., Ronnin Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: dfrisch@CLEMSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation of ESTs from tomato fruit tissue,
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                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
                                                                                                                                                                                                                                    /note-"Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhOI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

a 129 c 121 g 182 t
                                                                                                                                                                                                                                                                                                                                                          /clone_lib="tomato breaker
/tissue_type="Pericarp"
/dev_stage="breaker"
                                                                                                                                                                                                                                                                                                                                            /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                             /clone-"cLEG15H6"
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/cultivar="TA496"
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52.7%;
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Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronnning, C.M., Nierman, W., Fraser, C.M., Giovannoni, J.J., Martin, G.B. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW650280 518 bp mRNA EST 04-APR-
EST328734 tomato germinating seedlings, TAMU Lycopersicon
esculentum cDNA clone cLEI12F13 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                       Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
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100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                            Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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                                                                      134
                                                                                                                                                                                                                                                                                          dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                               sequence.
                                                               /Clone_lib="tomato germinating seedlings, TAMU"
/Lissue_type="whole seedlings"
/dev_stage="7 days post imbibtion"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; 7 days post imbibition on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
to two centimeters in seeds not showing obvious signs of
germination were discarded."
a 119 c 100 g 165 t
                                                                                                                                                                                          /organism="Lycopersicon
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEI12F13"
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AW616206
                                                                                                                                                                              Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 487)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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Lycopersicon hirsutum
                                                                                                                                                                                                                                                             Clemson University
100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                            Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                      Generation of ESTs from wild tomato (Lycopersicon hirsutum)
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                                                                                                                                                              sequence.
                   /organism="Lycopersicon
/db_xref="taxon:62890"
/clone="cLHT1D15"
                                                                                                       1. .487
                                                                                                                                Location/Qualifiers
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Best Local Similarity 51.7
Matches 246; Conservative
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Unpublished (1999)
Contact: David Frisch
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100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                      l (bases 1 to 497)
l (bases 1 to 497)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.
Alcala,J., Vrebalov,J., White,R., Bowman,C.L., Ahn,S., Ronning,C.
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sper
Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                likely with minor contaminations cells"
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/dev_stage="mixed stages"
                                                                                                                                                                                                                                                                                                                                                                        GI:8106335
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Pred. No. 1.5e-12;
0; Mismatches 230
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Best Local Simi
Matches 201;
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                                                                                                                                                                                                                                                                                                                                             ATCACTAAATTCGGAGGAGATGATGATTCTT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGAATAACG
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                                                                                                                                                                                                                                                                                                                         CTCCACAAATTCGGTGGACATGAACAATTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D.
                                                                                                                                                                                                 AW038515 490 bp mRNA
EST280198 tomato mixed elicitor,
clone cLET6D22, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: dfrisch@CLEMSON.
5 prime sequence
                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                      AW038515.1 GI:5897269
EST.
                                                                                                                                                                                       AW038515
                                                                                                                      Lycopersicon
                                                                                                                                        tomato.
                                                    (bases 1 to 490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
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a 106 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     harvested 3-5 days prior to ripening. Fruit were cut half to verify the seeds were indeed 'immature' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBlueScript SK(-); Site_1: EcoR1: Site_2:
Xho1: cLEF - Fruit were tagged at the 1cm stage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seeds and locules were discarded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lycopersicon
/cultivar="TA496"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="tomato fruit mature green, TAMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone-"cLEF42M23"
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No. 4.2e-08;
                                                                                                                                                                                                                      BTI Lycopersicon
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     Giovannoni
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REFERENCE
AUTHORS
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ORGANISM
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACTTCTTCCCCCTTTCATGCAATCTAATCTACCCTCTNTCGCCGGAGAAAATGCCGGAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACANTCCTTATCTCTAACCCTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGCCACCTCCCCACGGTGGCGCAGCTGAGCTAACGCTCCCTCTAACTTATTTTGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTGGTTTGTTTTTGGCTATATGCGTAGGATTTTATTCTACAAGCTATCGATTTCCAAA 123
                                                                                 Lycopersicon esculentum Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                    AW093479 409 bp mrNA
EST286659 tomato mixed elicitor,
clone cLET25A3, mrNA sequence.
AW093479 GI:6059074
         D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovan,J.
                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson,
Tel: 864 656 4366
Fax: 864 656 4293
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Clemson University
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Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prime sequence.
                                                                               (bases 1 to 409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; CLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="tomato mixed elicitor,
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
/clone="cLET6D22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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No. 8.
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                    and Giovannoni
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AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 TTCCGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGA 323
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                                                                                                                                                                                                                 sequence.
BE187619
                                                                                                                                                                                                                                                     BE187619
EST336180
Contact: VandenBosch K
                 1 (bases 1 to 788)
VandenBosch, K., Hur, J., Beremand, P., Peng, H. and Ellis, L.
ESTs from uninoculated seedling roots of Medicago truncatula
Unpublished (1999)
                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Medicago.
                                                                                                                                       Medicago truncatula
                                                                                                                                                                               EST
                                                                                                                                                             barrel medic.
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Fax: 864 656 4293
Email: dfr1sch@CLEMSON.EDU
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100 Jordan Hall, C
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Contact: David Frisch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; CLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2.6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
                                                                                                                                                                                                                                                       ΚVO
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/clone_lib="tomato mixed elicitor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon esculentum"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                      GCTTC 545
                                                                                                                                                                             TTGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGA
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TCTTC
                                                                          CTAGCTTTTCATCATGTTGCTGCTGATGGAAGAACCTTCCACAATTTCATCAAAACATGG
                                                                                                               ATAACGACGCACCACCGTTAGCGATGCTCCATCGTTTGTAGGGTTTATGAAGAGTTGG
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Texas A&M University
College Station, TX 77843-3258,
Tel: 409 845 7707
Fax: 409 845 2891
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Texas A&M University name:T260795e
TIGR sequence name:MTGAU50TK
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483
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR cells."
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/culfivar="genotype A17"
/db_xref="taxon.3880"
/clone="pkV0-1613"
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JOURNAL
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Best Local Similarity
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GTAACATCGTTTGGCCTTCGGATTCTCCTAAACCATTCCTCCAATTCAATCCAAATGATG
                                                        GCAATCTAATCTACCCTCTATCGCCGGAGAAAATGCCGGAGTTCCGGTATCAGAACGGTG
                                                                                                                                                            AGCTTCTCTTCTACGAACTCCCCTGTTCCAAACCCGCC-----TTCCTCGAAACCG 166
                                                                                                                                                                                                                                                                                                                                                                                                                         AGCAGTCACTCCCGCTCACCTTCTTCGACATGACGTGGCTGCATTTTCCACCCCATGCTTC 115
                                                                                                                           GTATTTTCTTCTACACCCTCCCAAGTTCACACTCACACCCCTACTTTTTCTTCGAAAATC 175
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Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sp
Eukaryota; Viridiplantae; Embryophyta; Contactoria; Tracheophyta; Sp
Eukaryota; Viridiplantae; Embryophyta; Contactoria; Tracheophyta; Sp
Eukaryota; Tracheophyta; Tracheoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              College Station, TX 77843-3258, Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
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TIGR sequence name: MTEBK10TK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VandenBosch,K., Hurt,J., Moore,J., Be
Town,C.D., Bowman,C.L., Craven,M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VandenBosch, K., Hurt, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      More information is available
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Seedling roots"
/dev_stage="3 days post-inocu
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
/culitivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV3-25A19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. coli strain SOLR"
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pKV3-25A19, mRNA
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., Holt,I.E. and
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                   AGCAGTCACTCCCGCTCACCTTCTTCGACATGACGTGGCTGCATTTTCCACCCCATGCTTC 115
AACTATCTCTCCCTCTCACATTTTTTGACTATATTTTGGCTAAGATTTCATCCGGTAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATGAAGAGTTGGGCTTCCATCACTAAATTCGGAGGA3A 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L (bases 1 to 656)
He,X.-Z., Shadle,G., S,C.J., Flores,H.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATCAAAGCATGGTCTTCTATATGTAAATCTCTTGAAGA 572
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                                                                                                                                                                                                                                                                                                                                                 Email: radixon@noble.org
Insert Length: 656 Std Error: 0.0
Plate: 056 row: D column: 05
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula stem library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula
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AW692527.1 GI:7567263
EST.
barrel medic.
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                                                                                     Similarity
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1: 580 221 7302
5: 580 221 7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Flores, H.R., Inman, J.T.,
                                                                                                                                                                                                                                /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF055D05ST"
/clone_lib="Developing stem"
/tissue_type="stem"
                                                                                                                                                              /dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture
internodal stem segments"
163 c 78 g 228 t
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                   5.2%;
49.9%;
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                                                                  Score 79; DB 24;
Pred. No. 1.4e-06;
0; Mismatches 250;
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Weller,J.W., May,G.D. and Dixon
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More information is available at.
'http://chrysie.tamu.edu/medicago'
Seq primer: Skmod (CTA gAA CTA gtg
Location/Qualifiers
                                                                                                                                                                                                                                        Email: mjharrison@noble.org
Noble EST name:N254013e
                                                                                                                                                                                                                                                                                                                                              Contact: Maria J. Harrison
Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                               Glomus versiforme
                                                                                                                                                                                                                                                                                                                                                                                                        Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M. ESTs from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula/Glomus versiforme Medicago truncatula/Glomus versiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW586972 677 bp mRNA EST 20-MAR-20 EST313595 MHAM Medicago truncatula/Glomus versiforme mixed library cDNA clone pMHAM-56M23, mRNA sequence.

AW586972
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                                                   /cultivar="Medicago truncatula genotype Al7"
/db_xref="taxon:119092"
/clone="ринам-56м23"
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38
                                       /clone_lib="MHAM"
                                                                                                            library"
                                                                                                                 organism="Medicago truncatula/Glomus versiforme mixed
                                                                                                                                                                                                                                                                                                   ogy Division Roberts Noble Foundation Ardmore, OK 73401,
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EST355090 tomato flower
     van
                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spe
Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                    Lycopersicon esculentum
                                                                                                                                                                              BE353747.1
                                                                                                                                          comato
                                         (bases 1 to 311)
der Hoeven,R.S., Bezzeredes,J.L., Hansen,T.S., Craven,M.B., Bowman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."

/lab_host="E. coli strain SOLR"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."

90 a 162 c 86 g 238 t l others
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49.98;
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No.
                                                                                                                                                                                                             clone cTOD5L6, mRNA
Bowman, C.L., Ronning
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Cornell University
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Ronning, C.M.,
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                                                                           Spermatophyta;
dae; euasterids
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACTCCCTCTTACTTATTTTGACCATGTTTGGTTAGGGTTTCGCCGTATGAGGCGGATAT
                                                                                                                                                                                                                                                                                                                                                                                                         AAAATGTACTCTCCCTCACTCTCAAACACTATACGCCCTTATCCGGAAACGTTGCTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 605)
Asamīzu,E., Nakamura,Y., Sato,S. a
A large scale analysis of cDNA in
of 12,028 non-redundant expressed
size-selected cDNA libraries
                                                                                                                                                                                                      AV440958 605 bp mRNA
AV440958 Arabidopsis thaliana
old Arabidopsis thaliana cDNA
AV440958
                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                       AV440958.1
EST.
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100 Jordan Hall, C
                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 864 656 4366
Fax: 864 656 4293
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Generation of
                                                                                                                                                         thale cress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="flower"
/tissue_type="anthesis"
/dev_stage="anthesis"
/note="Yector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4081"
/clone="cTOD5L6"
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/cultivar="TA496"
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57.1%;
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Pred. No.
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                                                                                                                                                                                                                      above-ground organ two to six-week clone AP217a04_f 3', mRNA sequence.
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3.6e-06;
                                                      and Tabata, S
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                   Arabidopsis thaliana: Generation sequence tags from normalized and
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BASE COUNT
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Search completed: October 20, 2000, 02:07:32 Job time: 1915 sec
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                                                                                                                                                             1208 AAGAGATACTGTCGATTGATGGAGAGAGTTTACGATGTCGTTGTGTAAACCGAGGGATG 1267
                                                                                                                                                                                                                                                                                                                                     1148 CGGGATCGAGGCTTGATCTTTACGGCGCGGATTTTGGATGGGGTAAGGCGGTGAAGC 1207
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                                                                                              81
                                                                                      ATTTGCTTCACAAGGGACTAGAAAATTAAATCATTTTTT 43
                                                                                                                                                                                                                                       TGGTGGTTGTCAATTGACCAAGGTGA---AGCGATTTCTTTTGCGGAGAGTAGAGATG
                                                                                                                           ATTATTTTGCGGAGGGAATAAAGGGTTGATTAATCATTT 1366
                                                                                                                                                                                                                                                                                                                  DNA Res. 7, 175-180 (2000)
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
The Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 605
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="APZ17404_f"
/clone_lib="Arabidopsis thaliana above-ground organ two to six-week old"
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/dev_stage="two to six-week old"
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1: sp_archea:*
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Listing first 45 summaries
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COnway A., Conway A., Kurtz D., Oji O., Osborne B., Shen
Toriumi M., Vysotskala V., Yu G., Davis R.W., Federspiel
Theologis A., Ecker J.R.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO00103; AAB61522.1; -
MENDEL; 16800; Arath; 2598;16800.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II;
Brassicaceae; Arabidopsis.
Arabidopsis thaliana (Mouse-ear cress).
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Plant J. 14:703-713(1998).
EMBL; AF053307; AAC99311.1; -.
TTANSFERASE; ACYLTRANSFERASE.
SEQUENCE 439 AA; 49873 MW; 1357C76550E0D
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STRAIN=CV. LITTLE DELICATA;
MEDLINE; 98346012.
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                                         Arabidopsis thaliana (Mouse-ear cress)
Eukaryota: Viridiplantae; Embryophyta;
                                                                                    F11C1.120.
                                                                                                       ANTHRANILATE
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                    Magnoliophyta;
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Conservative
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Bargues M., Collado M.C.
Mewes H.W., Lemcke K., 1
Submitted (NOV-1999) to
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SEQUENCE 4
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; Rosidae;
Brassicaceae; Arabidopsis.
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064470;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
PUTATIVE ANTHRANILATE N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE.
T20K24 8.
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Submitted (DEC-1999) to the
EMBL: AL132976; CAB62306.1;
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Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; Rosidae;
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01-MAY-2000 (TrEMBLrel. 13, Created)
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ANTHRANILATE N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE
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he EMBL/GenBank/DDBJ
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ne EMBL/GenBank/DDBJ
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/er K.F.X., (
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Pred. No.
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Brassicales;
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D P93094

C P93094;
C P93094;
C P93094;
OT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-WAY-1997 (TREMBLrel. 12, Last annotation update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE HYPOTHETICAL 50.8 KDA PROTEIN (FRAGMENT).
OS Cucumis melo (Muskmelon).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spe
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Cucy
Cucumbitaceae; Cucumis.
  RESULT P93094 AC PS OC COC MEE HY COC MEE HY
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Best Local S
Matches 6
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STRAIN-CV. CANTALOUPE CHARENTAIS; TISSUE-FRUIT;
STRAIN-CV. CANTALOUPE CHARENTAIS; TISSUE-FRUIT;
MEDLINE; 97188564.
Aggelis A., John I., Karvouni Z., Grierson D.;
"Characterization of two cDNA clones for mRNAs exi
ripening of melon (Cucumis melo L.) fruits.";
Plant Mol. Biol. 33:313-322(1997).
RMBL; 270521; CAA94432.1;
RMBL; 270521; CAA94432.1;
RMBLE; 10795; Cucume; 2594; 16795.
                                                                                                                                                                                                                                                                                      Q43583;
Q43583;
Q1-NOV-1996
Q1-NOV-1999
SEQUENCE FROM N.A. STRAIN-CV. BOTTOM MEDLINE; 96343929.
                                                                                                        Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Asteridae; euasterids
Solanaceae; Nicotiana.
                                                                                                                                                                                                                                   HSR201
HSR201.
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STRAIN-CV. COLUMBIA;

Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,

Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams

Somerville C.R., Venter J.C.;

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AC002392; AAD12025.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
NON_TER 1
SEQUENCE 455 AA; 5
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(TrEMBLrel. 12,
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I; Solanales;
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O48761;
O1-JUN-1998
O1-JUN-1998
O1-AUG-1998
F21B7.32.
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Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE.
Gentiana triflora.
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Submitted (JAN-1996) to the EMBL,
EMBL; X95343; CAA64636.1; -.
MENDEL; 16796; Nicta; 2594; 16796.
***COTTENCE 460 AA; 50972 MW; F
                         MEDLINE;
                                                     TISSUE-PETAL;
                                                                          SEQUENCE FROM
                                                                                                                          Magnoliophyta;
Gentianaceae;
                                                                                                                                                                     Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ecker J.R.;
Submitted (JAN-1998) to the
EMBL; AC002560; AAB97723.1;
SEQUENCE 461 AA; 52086 MW
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Conway A., Conway A.,
Vysotskaia V., Yu G.,
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"Characterization of hsr201 and hsr515, two tobacco genes preferentially expressed during the hypersensitive reactiby phytopathogenic bacteria.";
by phytopathogenic bacteria.";
plant Mol. Biol. 31:255-265(1996).
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnollophyta; eudicotyledons; Rosidae; eurosids II;
Brassicaceae; Arabidopsis.
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Oji O., Shen Y.K.,
., Federspiel N.A.,
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                                                        SEQUENCE FROM N.A.

Kikuchi Y., Shiokawa K., Morita I

Kikuchi Y., Shiokawa K., Morita I

Tipomoea batatas hcbt mRNA for N

Synthase, complete cds.";

Submitted (NOV-1999) to the EMBL,

EMBL; AB035183; BAA87043.1; -.
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Q9SST8;
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Eukaryota; Viridiplantae; Embryophyta; '
Magnoliophyta; eudicotyledons; Rosidae;
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Nam Y. W., Tichit L., Leperlier M., Cuerq B., I

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ

EMBL; AJ001450; CAA04771.1; -.

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SEQUENCE 99 AA; 11336 MW; 3B567A461709585
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EMBL; AB010708; CAB19224.1; -.
                                                                                                                                                                                                                                                                                                                     Ipomoea batatas (Sweet potato) (Batate).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Asteridae; euasterids
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01-MAY-2000 (TrEMBLrel. 13, Last annot
01-MAY-2001 (TrEMBLrel. 13, Last annot
N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE
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I; Solanales;
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ROUNDSLEY S.D., Ketchum K.A., Lin X., Phillips C.,
Fuhrmann J.L., White O., Kerlavage A.R., Adams M
Venter J.C.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ da
EMBL; AF002109; AAB95283.1; -.
MENDEL; 16798, Arath; 2596;16798.
Hypothetical protein.
SEQUENCE 482 AA; 52882 MW; 3C6341771A81989A
                                                                                                                                                                                                             081365;
01-NOV-1998
01-NOV-1998
01-MAY-2000
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004201;
01-JUL-1997
01-JUL-1997
01-NOV-1999
                                             Mbeguie-A-Mbeguie D., Fils-Lycaon B.;
Molecular cloning and partial nucleotide
containing protein from apricot.
Submitted (JUN-1998) to the EMBL/GenBank/D
EMBL; AF071893; AAC24587.1;
INTERPRO; IPRO01471;
PFAM; PF00847; AP2-domain; 1.
NON_TER
                                                                                                                                             Prunus
[1]
                                                                                                                                                             Prunus armeniaca (Apricot).
Eukaryota; Viridiplantae; Embryophyta; '
Magnoliophyta; eudicotyledons; Rosidae;
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Magnoliophyta; eudicotyle
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T29M21.14.
                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BERGERON; TISSUE-MESOCARP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta;
                                      SEQUENCE
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8 (TremBirel. 08, Last sequence up
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Arabidopsis.
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04, Last sequence update)
12, Last annotation update)
ROTEIN T29M21.14 IN CHROMOSOME
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43;
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Matches 5; Conservative
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EU Arabidopsis sequencing project;

EU Arabidopsis sequencing project;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AL133315; CAB62361.1; -.

Hypothetical protein.

SEQUENCE 430 AA; 48004 MW; 6210941B7C14BB31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Schoisne N., Robert C., Brottier P., Wincker P., Cattolico L.,
Choisne N., Robert C., Brottier P., Wincker P., Cattolico L.,
Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9SMM7 PRELIMINARY; PRT; 430 AA.
Q9SMM7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 48.0 KDA PROTEIN.
T8P19.230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Buagnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
Brassicaceae; Arabidopsis.
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Pred. No. 64;
1; Mismatches
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Title: Perfect score: Sequence:

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Scoring table:

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Copyright (c) 1993 - 2000 Compugen
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AF227981 Euphorbia
A16155 pTOM36. 10/
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AF053307 Catharant
AF190130 Taxus cus
AB029340 Perilla f
E12756 Perilla oci
E12757 Senecio cru
Z70521 C.melo mRNA
A65937 Sequence 1
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Anderson, J.V. and H
Direct Submission
                                                                                                                                                                                        Anderson, J.V. and Horvath, D.P. Identification of mRNAs expressed of Euphorbia esula (leafy spurge)
                                                                                                                                                                                                                               Euphorbia esula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Malpighiales; Euphorbiaceae; Euphorbia.
                                                                                                                                                                                                                                                                                                      AF227981 850 bp mRNA
Euphorbia esula F21J9.20-like
AF227981
                                                                                                                             Submitted (26-JAN-2000) Plant Science, USDA/ARS, 1605 Albrecht Blvd., Fargo, ND 58105, USA
                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                           leafy spurge
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                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="underground adventitious |
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/clone="12a"
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                   /codon_start=1
                                                                                                                    Location/Qualifiers
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                                                                                                                                                             Horvath, D.P
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AC017179 Drosophil
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                                                                                                                                                                                    Transformed tomato plants Patent: US 5569829-A 1 29-OCT-1996;
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Bird, C.R., Boniwell, J.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Madagascar periwinkle.
Catharanthus roseus
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AF053307
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1 (bases 1 to 1320)
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-Pierre,B., Laflamme,P. and De Luca,V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="deacetylvindoline 4-0-acetyltransferase"
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/db_xref="Gi:4091808"
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ADGGTIASFMKDWAASACYLSSSHHVPTPLLVSDSIFPRQDNIICEQFPTSKNCVEKY
ADGGTIASFMKDWAASACYLSSSHVPTPLTAFLSFCATVAGKSAKNNNCGOS,PFPV
LOAINLRPILELPQNSVGNLVSIYFFRTIKENDYLNEKETLVINELRKEKÖKIKNL
SREKLTYVAQMEEFYKSLKEFDISNFLDIDAYLSDSWCRFPFVDDFGMKFPIWVCLF
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QPYIKNCVVMMDYFFGDDYGIEAIVSFEQEKMSAFEKNEQLLQFVSN"
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/cultivar="Little Delicata"
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17-0-acetyltransferase"
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/EC_number="2.3.1.107"
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Location/Qualifiers
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76.5%;
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Pred. No. 7.7e+02;
2; Mismatches 2;
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Taxus cuspidata
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Conferopsida; Conferales; Taxaceae; Taxus.
                                              Sakakibara, K.Y., Tanaka, Y., Mizutani, M.F., Fujiwara, H
Ashikari, T., Yamaguchi, M. and Kusumi, T.
Molecular and biochemical characterization of a novel
hydroxycinnamoyl-CoA: anthocyanin 3-O-glucoside-6
Unpublished (199)
2 (bases 1 to 1476)
Sakakibara, K.Y., and Tanaka, Y.
                                                                                                                                                                                                                                            anthocyanin acyltransferase.
Perilla frutescens leaf cDNA to mRNA.
Perilla frutescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Walker, K., Schoendorf, A. and Croteau, R. Direct Submission
Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Sakakibara, Suntory Research Center, Fundamental Research, 1
                                   Direct Submission
                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Asteridae; euasterids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mektdlhvnliekvmvgpspplpkttlqlssidnlpgvrgsifn allivanspspmisadpaktplrealakilvvyppfagrlretengdleveggegam fleamadnelsvlgdeddsnpspgogllfslpldtnrkdlsllvvgvtreteggevygv sfhigvegaagelkglaemargevklslepimnrelyklddpkvlgpfffefelr psivekivgvfildfetinvikgsvmeeckefcssfevasamtwiarrafglese vkilfgmdmrnsfnpplpsgygnsigtacaddnvgdblsgsllraimiikkskvsl
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MQNYFLFLKPSKNKPDGIKILMFLPLSKMKSFKIEMEAMMKKYVAKV"
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76.5%;
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Perilla ocimoides mRN
E12756 GI:3251588
E12756.1 GI:3251588
JP 1997070290-A/4.
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PC (C12N9
PC strand
CC topolc
FH Key
FH Source
FT Source
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SUNTORY LTD
OS Perilla ocimoides
PN JP 1997070290-A/4
PD 18-MAR-1997
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AShikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y. Yonekura,K., Mizutani,M. and Kusumi,T. GEOLE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY Patent: JP 1997070290-A 4 18-MAR-1997;
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618-8503, Japan (E-mail:Keiko_Sakakibara@suntory.co.jp,
Tel:+81-75-962-8807, Fax:+81-75-962-8262)
Location/Qualifiers
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C12N15_09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 1479)
                                                                                                                      /organism='Perilla ocimoides'
/tissue_type='leaves'
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strandedness: Double;
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LKFPLQSRHPSLPTDRIRTTYVTTQSKIKKKKGWIQSKVPSLVBLSSFVAIAAYWWAG
ITKSFTADEDQDNEDAFFLIPVDLRPRLDPVPENYFGNCLSYALPRMRRELVGEKG
VFLAABVIAABIKKRINDKRILETVEKWSPEIRKALQKSYFSVAQSSKLDLYGADFGW
GKARKQEILSIDGEKYAMTLCKARDFEGGLEVCLSLPKDKMDAFAAYFSLGING"
19 a 315 c 331 g 411 t
                                                                                                                                                                          source
                                                                                                                                                                                                                                             topology: Linear;
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/product-'acyltransferase'
Location/Qualifiers
1. .1479
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/db_xref="taxon:48386"
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76.5%;
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                                                                               /clone='pSAT208'
1. .1343
                                                                                                                                                                                                                         Location/Qualifiers
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Pred. No. 7.6e+02;
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   C.melo mRNA (clone
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PC (C12NS
CC strand
CC topolt
FH Key
FT source
FT CDS
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070290-A 5 18-MAR-1997;
SUNTORY LTD
OS Senecio cruentus
PN JP 1997070290-A/5
PN JP 1997070290-A/5
PD 18-MAR-1997
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19
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PF 30-JAN-1996 JP 1996046534
PF 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 196915 PI
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU FUJIWARA HIROYUKI, PI NAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                              MASAHIRO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unclassified.
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Senecio cruentus mRNA
E12757 GI:3251589
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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strandedness: Double;
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Location/Qualifiers
1 1500
                                                                                                                                                                                                    /organism="unidentified"
/db_xref="taxon:32644"
293 c 296 g 47
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/db_xref="taxon:32644"
316 c 331 g 41
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1512 bp mku
(clone pMel2).
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76.5%;
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                                                                                                                                                                                                                                                                               /organism='Senecto cruentus'
/tissue_type='petal'
/clone='pCAT48'
1.1367
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                                                                                                                            Score 14.2; DE 5;
Pred. No. 7.6e+02;
2; Mismatches 2;
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Pred. No. 7.6e+02;
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polyA_signal
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Matches 13
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                                                                                                                       Sequence 1 from Patent A65937
                                                                                                                                                                                                                                                                                                                                                    ch 83.5%;
1 Similarity 76.5%;
13; Conservative
                                         unidentified unidentified
unclassified.
1 (bases 1 to 1526)
                                                                                                        A65937.1
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Submitted (01-APR-1996) John I., The University of Nottingham, Physiology and Environmental Science, Sutton Bonington Campus, Loughborough, United Kingdom, LE12 5RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aggelis, A., John, I., Karvouni, Z. and Grierson, Characterization of two cDNA clones for mRNAs ripening of melon (Cucumis melo L.) fruits Plant Mol. Biol. 33 (2), 313-322 (1997)
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/protdict="unknown"
/protdin_id="CAA94432.1"
/protdin_id="CAA94432.1"
/db_xref="GI:1843440"
/db_xref="GI:1843440"
/db_xref="GI:1843440"
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/translation="DESFHVRKCOPELIAPANPTPYEFKOLSDVDDQOSLRLQLPFVN
IYPHAPSLEGDDPKYVKEAIGKALVFYYPLAGRLREGPGRKLFVECTGEGFIFGLCFN
IYPHAPSLEGDDPKYVKEATGKALVFYYPLAGRALLTARDPPRITFRHYEYDOVVDM
KSGLIEVNSKIDQLEFFSGVGJISTLRQTFLPAHHLDGPSFEVLTAVWRLRTIALOFKP
EEEVRECVMNLRSKIDIPLGYYGNAVVVPAVITTAAKLCGNPLGYAVDLIRKAKAKA
TMEYIKSTVDLMVIKGRPYFTYVGSFMMSDLTRIGVENVDFGRGKAIFGGPTTTGARI
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QSASK*
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/clone_lib="Lambda UNI-ZAP"
<1. .1512
<1. .1370
                                                                                                     GI:4537934
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/cultivar="Cantaloupe charentais"
/db_xref="taxon:3656"
/clone="pMEL2"
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/tissue_type="fruit"
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I16758
                                                                             Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophyta; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.
                       Czernic,P., Huang,H.C. and Marco,Y. Czernic,P., Huang,H.C. and Marco,Y. two tobacco genes Characterization of hsr201 and hsr515, two tobacco genes preferentially expressed during the hypersensitive reaction provoked by phytopathogenic bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuttle,A.B. and CroSaland,L.D.
Anther-specific CDNA sequences, genrecumbinant DNA sequences
Patent: US 5477002-A 1 19-DEC-1995;
                                                                                                                                                                         N.tabacum mRNA for
X95343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
                                                                                                                                      hsr201 gene; hypersensitivity-related common tobacco.
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295 c 330 g
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297 c
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/db_xref="taxon:32644"
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TITLE
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                                                        THORS Ashikari, T., Tanaka, Y., Fujiwara, H., Nakao, M., Fukui, Y.,
YONGKURA,K., MIZUTANI,M. and Kusumi,T.

TLE GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 3 18-MAR-1997;
SUNTORY LTD
SUNTORY LTD
OS PETUNIA hybrida
PN JP 1997070290-A/3
PD 18-MAR-1997
PF 30-
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Petunia hybrida mRNA f
E12755 1 GI:3251587
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 MASAHIRO,
PI FUKU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submitted (12-JAN
                              PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU,
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FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC
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VKKTKSDVTEEYMKSVADLMYLKGRPHFTVVRTFLVSDVTRGGFGEVDFGWGKAVYGG
PAKGGVGAIPGVASFYIPFKNKKGENGIVVPICLPGFAMETFVKELDGMLKVDAPLVN
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/clone_lib="pBK phagemid vector"
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AZU, FUJIWARA HIROYUKI,
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Search completed: October 20, 2000, 03:37:59 Job time: 7317 sec
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ORIGIN
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83.5%; Score 14.2; DE 5; Length 1605;
Best Local Similarity 76.5%; Pred. No. 7.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0
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PC (C12N9/10,C12R1:19);
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CC topology: Linear;
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FT Key Location/Qualifiers
FT Source 1.1605
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FT CDS 67.1413
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"T Location/Qualifiers
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      Query
Match
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1703
     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-197-380-1
US-08-738-349-1
US-08-721-6080-9
PCT-US94-01782-9
US-08-726-160-1
PCT-US94-01782-1
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US-08-684-862-1
US-09-065-474-103
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TT 2 quence 1, Application US/08738349 Rent No. 5869638 ENERAL INFORMATION: APPLICANT: Takeshita, Sunao APPLICANT: Takeshita, Sunao APPLICANT: Kawai, Shinji APPLICANT: Kawai, Shinji APPLICANT: Tsujimura, Atsushi APPLICANT: House, Arsushi APPLICANT: Boon TITLE OF INVENTION: Bone-Related Cadherin-Like TITLE OF INVENTION: Process for Its Production NUMBER OF SEQUENCES: 12	Match 2.5%; Score 41.8; DB 5 ocal Similarity 63.4%; Pred. No. 0.026; s 64; Conservative 0; Mismatches 3 3 TGTTACGATAGGTATTGTATAATGCCATTATATATACTTCCAT	ESULT 1 S-09-197-380-1 Sequence 1, Application US/09197380 Patent No. 6096543 GENERAL INFORMATION: APPLICANT: Brett P. Monia APPLICANT: Lex M. Cowsert TITLE OF INVENTION: ANTISENSE MODULATION OF MEK1 FILE REFERENCE: RTS-0016 CURRENT APPLICATION NUMBER: US/09/197,380 CURRENT FILING DATE: 1998-11-20 NUMBER OF SEQ ID NOS: 47 SEQ ID NO 1 LENGTH: 2222 TYPE: DNA ORGANISM: Homo Sapiens FEATURE: NAME/KEY: CDS LOCATION: (73)(1254) S-09-197-380-1	36.6 2.1 937 2 US-09-031-485-3 36.6 2.1 937 2 US-08-847-429A-3 36.6 2.1 937 5 US-08-065-474-1 36.6 2.1 937 5 US-09-065-474-3 36.6 2.1 1029 2 US-09-031-485-6 36.6 2.1 1029 2 US-09-031-485-6 36.6 2.1 1029 2 US-09-031-485-3 36.6 2.1 1029 2 US-09-065-474-6 36.6 2.1 1029 5 US-09-065-474-8 36.6 2.1 1029 5 US-09-065-474-8 36.6 2.1 5235 2 US-09-031-485-35 36.6 2.1 5235 2 US-09-031-485-36 36.6 2.1 5235 2 US-09-065-474-35 36.6 2.1 5235 2 US-09-065-474-35 36.6 2.1 5235 2 US-09-031-485-32 36.6 2.1 5235 5 US-09-065-474-35 36.6 2.1 5235 5 US-09-065-474-35 36.6 2.1 5235 2 US-09-065-474-35
Protein and	;. Length 2222; 7; Indels 0; Gaps AAAGTATCCTATGCAATAG 1662	EXPRESSION	Sequence 3, Appli Sequence 1, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 8, Appli Sequence 8, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 36, Appli

CORRESPONDENCE ADDRESS:

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US-08-021-608D-9
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                                                                                                                                                                                                                                                Sequence 9, Application US/08021608D Patent No. 5580760
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 3581 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                          COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-408-4000
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                 STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                 2.3%;
Local Similarity 79.7%;
les 47; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Barker, M. P.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 25-OCT-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3315
                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                1015
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                                                                           NEW YORK
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                                                                                                        345 PARK AVENUE
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1300 I Street, N.W.
                                                             USA
IBM PC COMPATIBLE
                                                                                                                        MORGAN & FINNEGAN
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                FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA to mRNA
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Pred. No. 0.12;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3581;
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08726160 Patent No. 5734016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
           ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726
                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLACI
MOLECULE TYPE: CUI
HYPOTHETICAL: NO
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN,
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2320 TCAAAAAAAAAAAAAAAAAAAAAA 2347
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ORGANISM: Huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 22-FEB-19
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                          CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                 STREET:
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nes 57; Conserv
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OTHER INFORMATION:
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STRANDEDNESS: Double
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILLIAM S. FEILER
                                                                                                                                                                                                                 345 PARK AVENUE
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04-OCT-1996
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                                                                     PC-DOS/MS-DOS
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             US/08/726,160
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Pred. No. 0.24;
0; Mismatches 31;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 22-FEI CLASSIFICATION:

08/021,608

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GENERAL INFORMATION:
APPLICANT: THE GOV
APPLICANT: AS REPRI
APPLICANT: HEALTH
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REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.3%;
Best Local Similarity 64.8%;
Matches 57; Conservative
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HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
          PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
                                                                                     SOFTWARE: TOTAL CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PCT/US94/01782
                                                                                                                                                                                                                                    STREET: J. STREET: STREET: STREET YORK
CITY: NEW YORK
TABLE: NEW YORK
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: THE GOVERNMENT OF THE UNITED STATES
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
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                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2381

TYPE: Nucleic acid

STRANDEDNESS: Double

TOPOLOGY: Unknown
                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 22-FEB-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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CELL LINE: HL60
                                                                                                                                                                                                                        10154
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                                                                                                                                                                                                                                                                                        345 PARK AVENUE
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E: cDNA
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                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08021608D Patent No. 5580760
                                                                                                                                APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: WORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: cDI
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1676 ТСТТАЛЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 1703
                                                                                                                                                                                                                                                                                                                                                                                                                              2320 ТСАЛЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2260 AATGTATACTTTCACTTTCCAAATGCCTGTTTTGTGCTTTACAATAAATGATATGAAACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1616 ATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATG 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 20;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                      COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
OTHER INFORMATION: 470 bp variable
OTHER INFORMATION: region where R is A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNITS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANELLE:
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                                                                                                                          NEW YORK
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WORDPERFECT 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38.4; DB Pred. No. 0.24;
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Gaps

PRIOR APPLICATION DATA:

FILING DATE: 2: CLASSIFICATION: CURRENT APPLICATION DATA:

APPLICATION NUMBER:

22-FEB-1993

US/08/021,608D

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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-021-608D-1
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APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                     MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOPPY
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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CELL LINE:
FILING DATE: 0: CLASSIFICATION:
                                   APPLICATION NUMBER: US/08/726,160 FILING DATE: 04-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: NEW YORK STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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STRANDEDNESS: Double
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: Unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
APPLICATION NUMBER: U.S. FILING DATE: 22-FEB-1993 ATTORNEY/AGENT INFORMATION: NAME: WILLIAM S. FEILER
                                                                 PRIOR APPLICATION DATA:
                                                                                                                              SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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ORGANISM: Huma
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                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
                                                                              FILING DATE: 2:
CLASSIFICATION:
                                                                                                                                                                                                                                                                CITY: NEW YORK
STATE: NEW YORK
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                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                  345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                               THE GOVERNMENT OF THE UNITED STATES
AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
HEALTH AND HUMAN SERVICES
VENTION: NOVEL FUSE BINDING
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(212) /51-6849
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                                                                                                                                                                                                   FLOPPY DISK
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                                                                                                 22-FEB-1994
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variable region where R is A or
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; IDENTIFICATION METHOD:
; OTHER INFORMATION: 473 bp
; OTHER INFORMATION: variable region where R is
PCT-US94-01782-1
                                                                                                                                                                                                                                                                              Sequence 10, Application US/08684862 Patent No. 5759541 GENERAL INFORMATION:
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Best Local !
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APPLICANT:
APPLICANT:
                                                                     COMPUTER READABLE FORM:
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APPLICANT: Bialojan, Siegfried
TITLE OF INVENTION: No. 5759541el Proteins, the Preparation and Use
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                                                                                                                                                                           NUMBER OF SEQUENCES: 1
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CHROMOSOME/SEGMENT:
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       MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage COMPUTER: IBM AT-compatible, 80286 processor OPERATING SYSTEM: MS-DOS version 5.0 SOFTWARE: WordPerfect version 5.1
                                                                                        COUNTRY: USA
ZIP: 20036
                                                                                                                            STREET: 1101 Conf
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGTATACTTTCACTTTCCAAATGCCTGTTTTGTGCTTTACAATAAATGATATGAAACC 2322
APPLICATION DATA:
                                                                                                                   D.C
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                                                                                                                                           2: Keil & Weinkauf
1101 Connecticut Avenue
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(212) 75
                                                                                                                                                                                                                                                                  Bach, Alfred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38.4; DB Pred. No. 0.24;
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RESULT 10
US-09-065-474-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-JUL-1991
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 988 base pairs
TYPE: nucleic acid
STRANDENNES: cicleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6063599
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 102, Application US/09065474 Patent No. 6063599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
         REFERENCE/DOCKET NUMBER: HW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 102:
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, V.
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/065,474
FILING DATE: 24-APR-1998
                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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LOCATION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Carol Talkington Verser, ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/9 FILING DATE: 30-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Agkistrodon rhodostoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/684,862
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77.6%;
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                                                                                                                                                                                                                            Version 7.0
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MOLECULE TYPE: CDNA

STRANDEDNESS: si TOPOLOGY: linear

single

LENGTH: 184 nucleotides

nucleic acid

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Query Match
Best Local Similarity
Ches 66; Conserva
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US-09-065-474-103/c
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                                                                                                         ; STRANDEDNESS: sinc; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-09-065-474-103
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Best Local Similarity 57.48;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 103, Application US/09065474 Patent No. 6063599
                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION UNMER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970,493-772
TELEPHONE: 970,493-772
TELEPEAX: 970,484-9505
                                                                                                                                                                                                                                   TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Windows 95
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
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APPLICANT: Blehm, E. S
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1825 Sharp
CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Carol Talkington Verser, ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
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                                                                                                                                                                                               LENGTH:
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                    Conservative
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                                                                                                                                                            single
                                 2.18; 57.48;
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                               Score 36.6; DB Pred. No. 0.25;
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                Mismatches
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                                                  DB 5;
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                  49;
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                                                  Length 184;
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: 0
US-09-031-485-9
RESULT 13
US-09-031-485-10/c
; Sequence 10, Application US/09031485
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US-09-031-485-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1%;
Best Local Similarity 57.4%;
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APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/847,42
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION UNMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                     1102 CCATTGAAAAGAGGTTGCACAACGAAAAAGCCGTTCTTGCAGATGCAAAAACTTG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1042 CACATAAAGAGTTAGTTGGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAG 1101
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LENGTH: 810 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
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                                                                                                                                                                                                                                                                                                                                                                        224 CACAAGAACCGTTTTTTCAGCAAGTAGGGTATAATGGGACACCTGGAGATCCAGAAGAAC 283
                                                                                                                                                                                                               284
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CITY: Fort Collins
STATE: Colorado
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1825 Sharp Point Drive
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                                                                                               Sequence 9, Application US/08847429A
Patent No. 5827692
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blebm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: USES THEREOF
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Best Local S
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NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS.
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WordPerfect for Windows, Version 7.0 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1042 CACATAAAGAGTTAGTTGGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAG 1101
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APPLICATION NUMBER: US/0
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Blehm, E. Scot
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                                                                                                                                                                                                                                                                                                                                        527
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
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CITY: Fort Collins
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REFERENCE/DOCKET NUMBER: HW-5
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ZIP: 80525
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ADDRESSEE: Heska Corporation
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Best Local Similarity
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FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM For Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            STREET: 1820 .... STREET: Fort Collins
STATE: Colorado
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
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LENGTH: 810 nucleotide
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APPLICANT: Blehm, E. Scot
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STRANDEDNESS: single
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STATE: Colorado
                                           CLASSIFICATION:
                                                      APPLICATION NUMBER: US/0
FILING DATE: 24-APR-1997
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
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                                                                               US/08/847,429A
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REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
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